GenCore version 5.1.7


OM protein - protein search, using sw model

Run on: March 28, 2006, 11:16:29 ; Search time 29.5986 Seconds
(without alignments)
1661.969 Million cell updates/sec

Title: US-10-659-000-4
Perfect score: 3231
Sequence: 1 STIEEQAKTFLDKFNHEAED.....WLKDQNKNSFVGWSTDWSPY 595

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 3231 | 100.0 | 805 | 2 | US-08-989-299-2 | Sequence 2, Appli |
| 2 | 3231 | 100.0 | 805 | 2 | US-10-158-847-142 | Sequence 142, App |
| 3 | 3231 | 100.0 | 805 | 2 | US-09-407-427-2 | Sequence 2, Appli |
| 4 | 3231 | 100.0 | 805 | 2 | US-09-635-501-2 | Sequence 2, Appli |
| 5 | 3231 | 100.0 | 805 | 2 | US-09-635-501-106 | Sequence 106, App |
| 6 | 3231 | 100.0 | 805 | 2 | US-10-158-825-142 | Sequence 142, App |
| 7 | 3231 | 100.0 | 819 | 2 | US-09-949-016-11284 | Sequence 11284, A |
| 8 | 2987 | 92.4 | 681 | 2 | US-10-158-847-140 | Sequence 140, App |
| 9 | 2987 | 92.4 | 681 | 2 | US-10-158-825-140 | Sequence 140, App |
| 10 | 2987 | 92.4 | 711 | 2 | US-10-158-847-138 | Sequence 138, App |
| 11 | 2987 | 92.4 | 711 | 2 | US-10-158-825-138 | Sequence 138, App |
| 12 | 1335 | 41.3 | 732 | 1 | US-08-481-626-2 | Sequence 2, Appli |
| 13 | 1335 | 41.3 | 732 | 2 | US-08-989-299-4 | Sequence 4, Appli |
| 14 | 1335 | 41.3 | 732 | 2 | US-09-407-427-4 | Sequence 4, Appli |
| 15 | 1335 | 41.3 | 732 | 2 | US-09-635-501-4 | Sequence 4, Appli |
| 16 | 1335 | 41.3 | 1265 | 2 | US-09-964-899-19 | Sequence 19, Appl |
| 17 | 1335 | 41.3 | 1306 | 2 | US-08-989-299-7 | Sequence 7, Appli |
| 18 | 1335 | 41.3 | 1306 | 2 | US-09-407-427-7 | Sequence 7, Appli |
| 19 | 1335 | 41.3 | 1306 | 2 | US-09-635-501-7 | Sequence 7, Appli |
| 20 | 1334 | 41.3 | 732 | 2 | US-08-989-299-5 | Sequence 5, Appli |
| 21 | 1334 | 41.3 | 732 | 2 | US-09-407-427-5 | Sequence 5, Appli |
| 22 | 1334 | 41.3 | 732 | 2 | US-09-635-501-5 | Sequence 5, Appli |
| 23 | 1334 | 41.3 | 1312 | 2 | US-08-989-299-8 | Sequence 8, Appli |
| 24 | 1334 | 41.3 | 1312 | 2 | US-09-407-427-8 | Sequence 8, Appli |
| 25 | 1334 | 41.3 | 1312 | 2 | US-09-635-501-8 | Sequence 8, Appli |
| 26 | 1310 | 40.5 | 1313 | 2 | US-08-989-299-9 | Sequence 9, Appli |
| 27 | 1310 | 40.5 | 1313 | 2 | US-09-407-427-9 | Sequence 9, Appli |
| 28 | 1310 | 40.5 | 1313 | 2 | US-09-635-501-9 | Sequence 9, Appli |
| 29 | 1281 | 39.6 | 737 | 2 | US-08-989-299-6 | Sequence 6, Appli |
| 30 | 1281 | 39.6 | 737 | 2 | US-09-407-427-6 | Sequence 6, Appli |
| 31 | 1281 | 39.6 | 737 | 2 | US-09-635-501-6 | Sequence 6, Appli |
| 32 | 1281 | 39.6 | 1310 | 2 | US-08-989-299-10 | Sequence 10, Appl |
| 33 | 1281 | 39.6 | 1310 | 2 | US-09-407-427-10 | Sequence 10, Appl |
| 34 | 1281 | 39.6 | 1310 | 2 | US-09-635-501-10 | Sequence 10, Appl |
| 35 | 1073 | 33.2 | 615 | 2 | US-08-989-299-11 | Sequence 11, Appl |
| 36 | 1073 | 33.2 | 615 | 2 | US-09-407-427-11 | Sequence 11, Appl |
| 37 | 1073 | 33.2 | 615 | 2 | US-09-635-501-11 | Sequence 11, Appl |
| 38 | 989 | 30.6 | 694 | 2 | US-09-440-325A-1 | Sequence 1, Appli |
| 39 | 989 | 30.6 | 694 | 2 | US-09-846-996A-1 | Sequence 1, Appli |
| 40 | 989 | 30.6 | 694 | 2 | US-10-246-085A-1 | Sequence 1, Appli |
| 41 | 981 | 30.4 | 590 | 2 | US-09-902-540-10939 | Sequence 10939, A |
| 42 | 677 | 21.0 | 149 | 2 | US-09-621-976-3897 | Sequence 3897, Ap |
| 43 | 635.5 | 19.7 | 907 | 2 | US-08-989-299-12 | Sequence 12, Appl |
| 44 | 635.5 | 19.7 | 907 | 2 | US-09-407-427-12 | Sequence 12, Appl |
| 45 | 635.5 | 19.7 | 907 | 2 | US-09-635-501-12 | Sequence 12, Appl |

ALIGNMENTS

RESULT 1
US-08-989-299-2
; Sequence 2, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robinson, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E., Beth
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-025.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 805 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-989-299-2

Query Match 100.0%; Score 3231; DB 2; Length 805;
Best Local Similarity 100.0%; Pred. No. 2.8e-309;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
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Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
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Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180

Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

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Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540

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Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613


RESULT 2
US-10-158-847-142
; Sequence 142, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF557
;  CURRENT APPLICATION NUMBER: US/10/158,847
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/295,004
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-158-847-142

  Query Match           100.0%;  Score 3231;  DB 2;  Length 805;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-309;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
US-09-407-427-2
; Sequence 2, Application US/09407427
; Patent No. 6610497
; GENERAL INFORMATION:
;  APPLICANT:  Acton, Susan L.
;  APPLICANT:  Robison, Keith E.
;  TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG  AND THERAPEUTIC
;  TITLE OF INVENTION:  AND DIAGNOSTIC USES THEREFOR
;  FILE REFERENCE:  MNI-132CP2
;  CURRENT APPLICATION NUMBER: US/09/407,427
;  CURRENT FILING DATE:  1999-09-29
;  PRIOR APPLICATION NUMBER:  09/163,648
;  PRIOR FILING DATE:  1998-09-30
;  PRIOR APPLICATION NUMBER:  08/989,299
;  PRIOR FILING DATE:  1997-12-11
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-407-427-2

  Query Match           100.0%;  Score 3231;  DB 2;  Length 805;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-309;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180

Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

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Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
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Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
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RESULT 4
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; Sequence 2, Application US/09635501
; Patent No. 6884771
; GENERAL INFORMATION:
;  APPLICANT:  Acton, Susan L. et al.
;  TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
;  TITLE OF INVENTION:  DIAGNOSTIC USES THEREFOR
;  FILE REFERENCE:  MNI-132CP3
;  CURRENT APPLICATION NUMBER: US/09/635,501
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  09/407,427
;  PRIOR FILING DATE:  1999-09-29
;  PRIOR APPLICATION NUMBER:  09/163,648
;  PRIOR FILING DATE:  1998-09-30
;  PRIOR APPLICATION NUMBER:  08/989,299
;  PRIOR FILING DATE:  1997-12-11
;  NUMBER OF SEQ ID NOS:  107
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-635-501-2

  Query Match           100.0%;  Score 3231;  DB 2;  Length 805;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-309;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
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Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
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Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
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Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
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Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
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Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
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Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
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RESULT 5
US-09-635-501-106
; Sequence 106, Application US/09635501
; Patent No. 6884771
; GENERAL INFORMATION:
;  APPLICANT:  Acton, Susan L. et al.
;  TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
;  TITLE OF INVENTION:  DIAGNOSTIC USES THEREFOR
;  FILE REFERENCE:  MNI-132CP3
;  CURRENT APPLICATION NUMBER: US/09/635,501
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  09/407,427
;  PRIOR FILING DATE:  1999-09-29
;  PRIOR APPLICATION NUMBER:  09/163,648
;  PRIOR FILING DATE:  1998-09-30
;  PRIOR APPLICATION NUMBER:  08/989,299
;  PRIOR FILING DATE:  1997-12-11
;  NUMBER OF SEQ ID NOS:  107
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 106
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-635-501-106

  Query Match           100.0%;  Score 3231;  DB 2;  Length 805;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-309;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
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Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378
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Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613


RESULT 6
US-10-158-825-142
; Sequence 142, Application US/10158825
; Patent No. 6900033
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF555
;  CURRENT APPLICATION NUMBER: US/10/158,825
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/294,976
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-158-825-142

  Query Match             100.0%;  Score 3231;  DB 2;  Length 805;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-309;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613


RESULT 7
US-09-949-016-11284
; Sequence 11284, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11284
;   LENGTH: 819
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-11284

  Query Match             100.0%;  Score 3231;  DB 2;  Length 819;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-309;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 92

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 152

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 212

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 272

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 332

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 392

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 452

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 512

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        513 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 572

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 627


RESULT 8
US-10-158-847-140
; Sequence 140, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF557
;  CURRENT APPLICATION NUMBER: US/10/158,847
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/295,004
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
;   LENGTH: 681
;   TYPE: PRT
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (219)..(219)
;   OTHER INFORMATION: Xaa equals any amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (240)..(240)
;   OTHER INFORMATION: Xaa equals any amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (499)..(499)
;   OTHER INFORMATION: Xaa equals any amino acid
US-10-158-847-140

  Query Match            92.4%;  Score 2987;  DB 2;  Length 681;
  Best Local Similarity  99.3%;  Pred. No. 2.5e-285;
  Matches  548;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         44 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 60

Qy        104 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 120

Qy        164 EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 180

Qy        224 AYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 283
              |||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        181 AYVRPKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYXLTVPFGQKPNIDVTDAMVDQX 240

Qy        284 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 300

Qy        344 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360

Qy        404 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 420

Qy        464 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 480

Qy        524 CDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 583
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        481 CDISNSTEAGQKLFNMLRXGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 540

Qy        584 SFVGWSTDWSPY 595
              ||||||||||||
Db        541 SFVGWSTDWSPY 552


RESULT 9
US-10-158-825-140
; Sequence 140, Application US/10158825
; Patent No. 6900033
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF555
;  CURRENT APPLICATION NUMBER: US/10/158,825
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/294,976
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
;   LENGTH: 681
;   TYPE: PRT
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (219)..(219)
;   OTHER INFORMATION: Xaa equals any amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (240)..(240)
;   OTHER INFORMATION: Xaa equals any amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (499)..(499)
;   OTHER INFORMATION: Xaa equals any amino acid
US-10-158-825-140

  Query Match            92.4%;  Score 2987;  DB 2;  Length 681;
  Best Local Similarity  99.3%;  Pred. No. 2.5e-285;
  Matches  548;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         44 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 60

Qy        104 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 120

Qy        164 EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 180

Qy        224 AYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 283
              |||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        181 AYVRPKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYXLTVPFGQKPNIDVTDAMVDQX 240

Qy        284 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 300

Qy        344 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360

Qy        404 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        361 GLLSPDFQEDNETEINPLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 420

Qy        464 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 480

Qy        524 CDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 583
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        481 CDISNSTEAGQKLFNMLRXGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 540

Qy        584 SFVGWSTDWSPY 595
              ||||||||||||
Db        541 SFVGWSTDWSPY 552


RESULT 10
US-10-158-847-138
; Sequence 138, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF557
;  CURRENT APPLICATION NUMBER: US/10/158,847
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/295,004
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 138
;   LENGTH: 711
;   TYPE: PRT
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (219)..(219)
;   OTHER INFORMATION: Xaa equals any amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (240)..(240)
;   OTHER INFORMATION: Xaa equals any amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (499)..(499)
;   OTHER INFORMATION: Xaa equals any amino acid
US-10-158-847-138

  Query Match            92.4%;  Score 2987;  DB 2;  Length 711;
  Best Local Similarity  99.3%;  Pred. No. 2.7e-285;
  Matches  548;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         44 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 60

Qy        104 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 120

Qy        164 EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 180

Qy        224 AYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 283
              |||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        181 AYVRPKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYXLTVPFGQKPNIDVTDAMVDQX 240

Qy        284 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 300

Qy        344 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360

Qy        404 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 420

Qy        464 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 480

Qy        524 CDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 583
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        481 CDISNSTEAGQKLFNMLRXGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 540

Qy        584 SFVGWSTDWSPY 595
              ||||||||||||
Db        541 SFVGWSTDWSPY 552


RESULT 11
US-10-158-825-138
; Sequence 138, Application US/10158825
; Patent No. 6900033
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF555
;  CURRENT APPLICATION NUMBER: US/10/158,825
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/294,976
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 138
;   LENGTH: 711
;   TYPE: PRT
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (219)..(219)
;   OTHER INFORMATION: Xaa equals any amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (240)..(240)
;   OTHER INFORMATION: Xaa equals any amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (499)..(499)
;   OTHER INFORMATION: Xaa equals any amino acid
US-10-158-825-138

  Query Match            92.4%;  Score 2987;  DB 2;  Length 711;
  Best Local Similarity  99.3%;  Pred. No. 2.7e-285;
  Matches  548;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         44 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 60

Qy        104 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 120

Qy        164 EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 180

Qy        224 AYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 283
              |||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        181 AYVRPKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYXLTVPFGQKPNIDVTDAMVDQX 240

Qy        284 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        241 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 300

Qy        344 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360

Qy        404 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 420

Qy        464 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 480

Qy        524 CDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 583
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        481 CDISNSTEAGQKLFNMLRXGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 540

Qy        584 SFVGWSTDWSPY 595
              ||||||||||||
Db        541 SFVGWSTDWSPY 552


RESULT 12
US-08-481-626-2
; Sequence 2, Application US/08481626
; Patent No. 5801040
;  GENERAL INFORMATION:
;    APPLICANT:  Soubrier, Florent
;    APPLICANT:  Alhenc-Gelas, Francois
;    APPLICANT:  Hubert, Christine
;    APPLICANT:  Corvol, Pierre
;    TITLE OF INVENTION:  Nucleic Acid Coding for the Human
;    TITLE OF INVENTION:  Testicular Angiotensin Converting Enzyme (ACE) and its
;    TITLE OF INVENTION:  Uses, Especially for the In Vitro Screening for this
;    TITLE OF INVENTION:  Enzyme in the Organism
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W., Suite 700
;      CITY:  Washington
;      STATE:  D.C.
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,626
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/656,183
;      FILING DATE:  04-MAR-1991
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 89-09062
;      FILING DATE:  05-JUL-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  04958-0006-02000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  732 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-481-626-2

  Query Match             41.3%;  Score 1335;  DB 1;  Length 732;
  Best Local Similarity   41.9%;  Pred. No. 2.4e-122;
  Matches  254;  Conservative  116;  Mismatches  202;  Indels   34;  Gaps    9;

Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE--------NVQNMNNAGDKWSA 53
              | | :|  |:::::  :: :: : : |:||||||| |         |:|  |:
Db         70 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT------ 123

Qy         54 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 113
                 :  | |: : : ::|| |:|  :: :|    : |   : :  | ||  | | ||
Db        124 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 181

Qy        114 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 173
              ||:|:    || ||| |  :|| |  | : ||||| || : |: :   | :|| | |: |
Db        182 VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 239

Qy        174 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 233
              | | | | || ||  ||   ::          :|:|  |:|::||| :|||||  |
Db        240 RLNGYVDAGDSWRSMYETPSLE----------QDLERLFQELQPLYLNLHAYVRRALHRH 289

Qy        234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 292
              |   :|:  | :|||||:|| : |:|:| | |||    |::| |:||: | |  :|:|||
Db        290 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 349

Qy        293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
              |: || |:||  :   ||  |||  | : :: ||| :|||    | ||||  || | ::|
Db        350 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 409

Qy        352 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
              : |||||||||| | |    |  || ||| |||||:|::::|| :|||||  |: ||| :
Db        410 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 469

Qy        412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
              | | :||||:| ||  :  :||:|:::|||  || | | |: : ::|| :: :  |:
Db        470 SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 528

Qy        472 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 531
              |||  :   || : ||: :   :|||:  : |||| ||||||| | ||||||||  | |
Db        529 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 588

Qy        532 AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 588
              |||:|   ::|| | ||  |:: : |  ||:   :|:||:||  ||: :|:     :||
Db        589 AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 648

Qy        589 STDWSP 594
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Db        649 QYNWTP 654


RESULT 13
US-08-989-299-4
; Sequence 4, Application US/08989299
; Patent No. 6194556
;  GENERAL INFORMATION:
;    APPLICANT:  Acton, Susan L.
;    APPLICANT:  Robinson, Keith E.
;    TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG
;    TITLE OF INVENTION:  AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/989,299
;      FILING DATE:  11-DEC-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold E., Beth
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  MIA-025.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  732 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-989-299-4

  Query Match             41.3%;  Score 1335;  DB 2;  Length 732;
  Best Local Similarity   41.9%;  Pred. No. 2.4e-122;
  Matches  254;  Conservative  116;  Mismatches  202;  Indels   34;  Gaps    9;

Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE--------NVQNMNNAGDKWSA 53
              | | :|  |:::::  :: :: : : |:|||||||| |         |:|  |:
Db         70 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT------ 123

Qy         54 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 113
                :  | |: : : ::|| |:|  :: :|    : |   : :  | ||  | | ||
Db        124 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 181

Qy        114 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 173
              ||:|:    || ||| |  :|| |  | : ||||| || : |: :   | :|| | |: |
Db        182 VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 239

Qy        174 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 233
              | | | | || ||  ||   ::          :|:|  |:|::||| :||||||  |
Db        240 RLNGYVDAGDSWRSMYETPSLE----------QDLERLFQELQPLYLNLHAYVRRALHRH 289

Qy        234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 292
              |   :|:  | :||||||:|| : |:|:| | |||   |::| |:||: | |  :|:|||
Db        290 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 349

Qy        293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
              |: || |:||  :   ||  |||  | : :: ||| :|||   | ||||  || | ::|
Db        350 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 409

Qy        352 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
              : |||||||||| | |   |  || ||| |||||:|::::|| :|||| |: ||| :
Db        410 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 469

Qy        412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
              | | :||||:| ||  :  :||:|::::||| || | | |: : ::|| :: :  |:
Db        470 SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 528

Qy        472 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 531
              |||  :   || : ||: :  :|||:  : |||| ||||||| | ||||||||  | |
Db        529 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 588

Qy        532 AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 588
              |||:|   ::|| | ||  |:: :  | ||:  :|:||:||  ||: :|:     :||
Db        589 AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 648

Qy        589 STDWSP 594
                :|:|
Db        649 QYNWTP 654


RESULT 14
US-09-407-427-4
; Sequence 4, Application US/09407427
; Patent No. 6610497
; GENERAL INFORMATION:
;  APPLICANT:  Acton, Susan L.
;  APPLICANT:  Robison, Keith E.
;  TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG  AND THERAPEUTIC
;  TITLE OF INVENTION:  AND DIAGNOSTIC USES THEREFOR
;  FILE REFERENCE:  MNI-132CP2
;  CURRENT APPLICATION NUMBER: US/09/407,427
;  CURRENT FILING DATE:  1999-09-29
;  PRIOR APPLICATION NUMBER:  09/163,648
;  PRIOR FILING DATE:  1998-09-30
;  PRIOR APPLICATION NUMBER:  08/989,299
;  PRIOR FILING DATE:  1997-12-11
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 732
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-407-427-4

  Query Match             41.3%;  Score 1335;  DB 2;  Length 732;
  Best Local Similarity   41.9%;  Pred. No. 2.4e-122;
  Matches  254;  Conservative  116;  Mismatches  202;  Indels   34;  Gaps    9;

Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE--------NVQNMNNAGDKWSA 53
              | | :|  |:::::  :: :: : : |:|||||||| |         |:|  |:
Db         70 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT------ 123

Qy         54 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 113
                :  | |: : : ::|| |:|  :: :|    : |   : :  | ||  | | ||
Db        124 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 181

Qy        114 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 173
              ||:|:    || ||| |  :|| |  | : ||||| || : |: :   | :|| | |: |
Db        182 VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 239

Qy        174 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 233
              | | | | || ||  ||   ::          :|:|  |:|::||| :||||||  |
Db        240 RLNGYVDAGDSWRSMYETPSLE----------QDLERLFQELQPLYLNLHAYVRRALHRH 289

Qy        234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 292
              |   :|:  | :||||||:|| : |:|:| | |||   |::| |:||: | |  :|:|||
Db        290 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 349

Qy        293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
              |: || |:||  :   ||  |||  | : :: ||| :|||   | ||||  || | ::|
Db        350 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 409

Qy        352 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
              : |||||||||| | |   |  || ||| |||||:|::::|| :|||| |: ||| :
Db        410 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 469

Qy        412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
              | | :||||:| ||  :  :||:|::::||| || | | |: : ::|| :: :  |:
Db        470 SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 528

Qy        472 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 531
              |||  :   || : ||: :  :|||:  : |||| ||||||| | ||||||||  | |
Db        529 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 588

Qy        532 AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 588
              |||:|   ::|| | ||  |:: :  | ||:  :|:||:||  ||: :|:     :||
Db        589 AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 648

Qy        589 STDWSP 594
                :|:|
Db        649 QYNWTP 654


RESULT 15
US-09-635-501-4
; Sequence 4, Application US/09635501
```

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; Patent No. 6884771
; GENERAL INFORMATION:
;  APPLICANT:  Acton, Susan L. et al.
;  TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
;  TITLE OF INVENTION:  DIAGNOSTIC USES THEREFOR
;  FILE REFERENCE:  MNI-132CP3
;  CURRENT APPLICATION NUMBER: US/09/635,501
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  09/407,427
;  PRIOR FILING DATE:  1999-09-29
;  PRIOR APPLICATION NUMBER:  09/163,648
;  PRIOR FILING DATE:  1998-09-30
;  PRIOR APPLICATION NUMBER:  08/989,299
;  PRIOR FILING DATE:  1997-12-11
;  NUMBER OF SEQ ID NOS:  107
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 732
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-635-501-4

  Query Match             41.3%;  Score 1335;  DB 2;  Length 732;
  Best Local Similarity   41.9%;  Pred. No. 2.4e-122;
  Matches  254;  Conservative  116;  Mismatches  202;  Indels   34;  Gaps    9;

Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE--------NVQNMNNAGDKWSA 53
              | | :|  |:::::  :: :: : : |:|||||||| |         |:|  |:
Db         70 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT------ 123

Qy         54 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 113
                :  | |: : : ::|| |:|  :: :|    : |   : :  | ||  | | ||
Db        124 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 181

Qy        114 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 173
              ||:|:    || ||| |  :|| |  | : ||||| || : |: :   | :|| | |: |
Db        182 VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 239

Qy        174 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 233
              | | | | || ||  ||   ::          :|:|  |:|::||| :||||||  |
Db        240 RLNGYVDAGDSWRSMYETPSLE----------QDLERLFQELQPLYLNLHAYVRRALHRH 289

Qy        234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 292
              |   :|:  | :|||||:|| : |:|:| | |||   |::| |:||: | |  :|:|||
Db        290 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 349

Qy        293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
              |: || |:||  :   ||  |||  | : :: ||| :|||   | ||||  || | ::|
Db        350 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 409

Qy        352 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
              : |||||||||| | |   |  || ||| |||||:|::::|| :|||||  |: ||| :
Db        410 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 469

Qy        412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
              | | :||||:| ||  :  :||:|:::::||| || | | |: : ::|| :: :  |:
Db        470 SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 528

Qy        472 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 531
              |||  :   || : ||: :   :|||:   : |||| ||||||| | ||||||||  | |
Db        529 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 588

Qy        532 AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 588
              |||:|   ::|| | ||  |:: : |  ||:   :|:||:||  ||: :|:     :||
Db        589 AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 648

Qy        589 STDWSP 594
                :|:|
Db        649 QYNWTP 654


Search completed: March 28, 2006, 11:18:49
Job time : 30.5986 secs
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GenCore version 5.1.7


OM protein - protein search, using sw model

Run on: March 28, 2006, 11:02:42 ; Search time 135.885 Seconds
(without alignments)
1923.914 Million cell updates/sec

Title: US-10-659-000-4
Perfect score: 3231
Sequence: 1 STIEEQAKTFLDKFNHEAED.....WLKDQNKNSFVGWSTDWSPY 595

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 3231 | 100.0 | 595 | 8 | ADO15670 | Ado15670 Human ACE |
| 2 | 3231 | 100.0 | 771 | 8 | ABM85139 | Abm85139 Human dia |
| 3 | 3231 | 100.0 | 805 | 3 | AAY84562 | Aay84562 A human a |
| 4 | 3231 | 100.0 | 805 | 3 | AAY67310 | Aay67310 Human MPR |
| 5 | 3231 | 100.0 | 805 | 4 | AAB48095 | Aab48095 Human Zac |
| 6 | 3231 | 100.0 | 805 | 4 | AAY72667 | Aay72667 Human ang |
| 7 | 3231 | 100.0 | 805 | 5 | AAE20353 | Aae20353 Human ACE |
| 8 | 3231 | 100.0 | 805 | 5 | ABG77011 | Abg77011 Human ang |
| 9 | 3231 | 100.0 | 805 | 5 | ABG77023 | Abg77023 Human ang |
| 10 | 3231 | 100.0 | 805 | 5 | AAU99701 | Aau99701 Human ang |
| 11 | 3231 | 100.0 | 805 | 6 | ABU07731 | Abu07731 Human zin |
| 12 | 3231 | 100.0 | 805 | 6 | ADA03344 | Ada03344 Human ang |
| 13 | 3231 | 100.0 | 805 | 6 | ABR56712 | Abr56712 Human ACE |
| 14 | 3231 | 100.0 | 805 | 7 | ADL95395 | Adl95395 Human ang |
| 15 | 3231 | 100.0 | 805 | 7 | ADL95494 | Adl95494 Human ang |
| 16 | 3231 | 100.0 | 805 | 8 | ADH51357 | Adh51357 Human ang |
| 17 | 3231 | 100.0 | 805 | 8 | ADO55144 | Ado55144 Protein # |
| 18 | 3231 | 100.0 | 805 | 9 | ADZ27233 | Adz27233 Human ACE |
| 19 | 3227 | 99.9 | 805 | 7 | ADC38728 | Adc38728 Human sec |
| 20 | 3218 | 99.6 | 702 | 9 | ADZ27234 | Adz27234 Soluble h |
| 21 | 2998.5 | 92.8 | 768 | 8 | ABM85140 | Abm85140 Human dia |
| 22 | 2987 | 92.4 | 681 | 6 | ADA03342 | Ada03342 Human ang |
| 23 | 2987 | 92.4 | 681 | 6 | ABR56711 | Abr56711 Human ACE |
| 24 | 2987 | 92.4 | 711 | 4 | AAU09092 | Aau09092 Novel hum |
| 25 | 2987 | 92.4 | 711 | 6 | ADA03340 | Ada03340 Human ang |
| 26 | 2987 | 92.4 | 711 | 6 | ABR56709 | Abr56709 Human ACE |
| 27 | 2897 | 89.7 | 555 | 4 | AAU12207 | Aau12207 Human PRO |
| 28 | 2897 | 89.7 | 555 | 6 | ABO17651 | Abo17651 Novel hum |
| 29 | 2897 | 89.7 | 555 | 6 | ABU80905 | Abu80905 Human PRO |
| 30 | 2897 | 89.7 | 555 | 6 | ABU66605 | Abu66605 Human PRO |
| 31 | 2897 | 89.7 | 555 | 6 | ABU59686 | Abu59686 Novel sec |
| 32 | 2897 | 89.7 | 555 | 6 | ABO24876 | Abo24876 Human sec |
| 33 | 2897 | 89.7 | 555 | 6 | ABU66881 | Abu66881 Human sec |
| 34 | 2897 | 89.7 | 555 | 6 | ADA45591 | Ada45591 Novel hum |
| 35 | 2897 | 89.7 | 555 | 6 | ADA76022 | Ada76022 Human PRO |
| 36 | 2897 | 89.7 | 555 | 6 | ADA18672 | Ada18672 Human PRO |
| 37 | 2897 | 89.7 | 555 | 6 | ADA61295 | Ada61295 Homo sapi |
| 38 | 2897 | 89.7 | 555 | 6 | ADB19080 | Adb19080 Novel hum |
| 39 | 2897 | 89.7 | 555 | 6 | ADB27621 | Adb27621 Human PRO |
| 40 | 2897 | 89.7 | 555 | 6 | ADA86100 | Ada86100 Novel hum |
| 41 | 2897 | 89.7 | 555 | 6 | ADB15664 | Adb15664 Human PRO |
| 42 | 2897 | 89.7 | 555 | 6 | ADA47450 | Ada47450 Human PRO |
| 43 | 2897 | 89.7 | 555 | 6 | ADA67245 | Ada67245 Human PRO |
| 44 | 2897 | 89.7 | 555 | 6 | ADB30252 | Adb30252 Human PRO |
| 45 | 2897 | 89.7 | 555 | 6 | ADA85548 | Ada85548 Novel hum |

ALIGNMENTS

RESULT 1
ADO15670
ID ADO15670 standard; protein; 595 AA.
XX
AC ADO15670;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human ACE2, SEQ ID 4.
XX
KW protein co-ordinate data; crystal;
KW angiotensin-converting enzyme-related carboxypeptidase; ACE2;
KW angiotensin-converting enzyme; ACE; enzyme.
XX
OS Homo sapiens.
XX
PN WO2004023270-A2.
XX
PD 18-MAR-2004.
XX
PF 09-SEP-2003; 2003WO-US028374.
XX
PR 09-SEP-2002; 2002US-0410010P.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Pantoliano MW, Ryan MD, Staker BL, Prasad GS, Tang J, Menon SP;
PI Towler PS, Williams DH, Fisher M;
XX
DR WPI; 2004-315606/29.
XX
PT Crystal of angiotensin-converting enzyme-related carboxypeptidase or its
PT homolog, useful for detecting compounds e.g. ligands capable of binding
PT to angiotensin-converting enzyme-related carboxypeptidase.
XX
PS Claim 6; Fig 4; 539pp; English.
XX
CC The present invention relates to a crystal (I) comprising an angiotensin-
CC converting enzyme-related carboxypeptidase (ACE2) or its homolog. (I) is
CC useful for detecting chemical compounds such as ligand, antagonist,
CC agonist, inhibitor, antibody, peptide, protein or drug having capability
CC of binding to the active site of the ACE2 protein. The present sequence
CC is human ACE2, used to illustrate the invention.
XX
SQ Sequence 595 AA;

Query Match 100.0%; Score 3231; DB 8; Length 595;

```
  Best Local Similarity   100.0%;  Pred. No. 3.8e-288;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595


RESULT 2
ABM85139
ID   ABM85139 standard; protein; 771 AA.
XX
AC   ABM85139;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:5388.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN43791.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 771 AA;

  Query Match             100.0%;  Score 3231;  DB 8;  Length 771;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-288;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558
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Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
```

RESULT 3
AAY84562
ID AAY84562 standard; protein; 805 AA.
XX
AC AAY84562;
XX
DT 25-JUL-2000 (first entry)
XX
DE A human angiotensin converting enzyme-2 (ACE-2) protein.
XX
KW Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
KW chronic heart failure; acute heart failure; myocardial infarction;
KW renal failure.
XX
OS Homo sapiens.
XX

| FH | Key | Location/Qualifiers |
|---|---|---|
| FT | Peptide | 1. .18 |
| FT | | /note= "signal sequence" |
| FT | Domain | 19. .740 |
| FT | | /note= "extracellular domain" |
| FT | Domain | 374. .378 |
| FT | | /note= "minimal zinc binding domain" |
| FT | Domain | 741. .765 |
| FT | | /note= "transmembrane domain" |
| FT | Domain | 766. .805 |
| FT | | /note= "cytoplasmic domain" |

XX
PN WO200018899-A2.
XX
PD 06-APR-2000.
XX
PF 29-SEP-1999; 99WO-US022976.
XX
PR 30-SEP-1998; 98US-00163648.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Acton LS, Robison KE, Hsieh FY;
XX
DR WPI; 2000-293140/25.
DR N-PSDB; AAA12764.
XX
PT Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
PT polypeptide useful for detecting an ACE-2 therapeutic for treating
PT hypertension, congestive heart failure, myocardial infarction,
PT atherosclerosis and renal failure.
XX
PS Claim 2; Fig 1; 138pp; English.
XX
CC The present sequence represents a human angiotensin converting enzyme-2
CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
CC sequence of the full length ACE-2 cDNA was determined from a clone
CC obtained from a cDNA library prepared from mRNA of a human heart of a
CC subject who had congestive heart failure. ACE-2 has significant sequence
CC homologies with ACE enzymes, and has also been shown to hydrolyse
CC angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
CC blood pressure related diseases and conditions, such as hypertension,
CC congestive heart failure, chronic heart failure, acute heart failure,
CC myocardial infarction, atherosclerosis and renal failure
XX
SQ Sequence 805 AA;

Query Match 100.0%; Score 3231; DB 3; Length 805;
Best Local Similarity 100.0%; Pred. No. 6.1e-288;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
```

RESULT 4
AAY67310
ID AAY67310 standard; protein; 805 AA.
XX
AC AAY67310;
XX
DT 11-APR-2000 (first entry)
XX
DE Human MPROT15 amino acid sequence #1.
XX
KW MPROT15; treatment; hypertension; human; myocardial disease; apoplexy;
KW heart disease; apoplexy; heart disease; nervous denaturation; hormone;
KW Alzheimer's disease; cytokine.
XX
OS Homo sapiens.
XX
PN JP11318472-A.
XX
PD 24-NOV-1999.
XX
PF 22-JAN-1999; 99JP-00014949.
XX
PR 13-MAY-1998; 98GB-00010373.
PR 18-AUG-1998; 98GB-00018009.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
DR WPI; 2000-109268/10.
DR N-PSDB; AAZ59465.
XX
PT MPROT15 polypeptide and MPROT15 polynucleotides - useful for the

PT treatment of hypertension, myocardial diseases, apoplexy, heart diseases,
PT nervous denaturation, Alzheimer's disease etc.
XX
PS Claim 1; Page 15; 22pp; Japanese.
XX
CC This is amino acid sequence #1 of human MPROT15. The MPROT15
CC polynucleotide and polypeptide sequences can be used for the treatment of
CC hypertension, myocardial diseases, apoplexy, heart diseases, nervous
CC denaturation, Alzheimer's disease and diseases related to the processing
CC of peptide hormones and cytokines
XX
SQ Sequence 805 AA;

Query Match 100.0%; Score 3231; DB 3; Length 805;
Best Local Similarity 100.0%; Pred. No. 6.1e-288;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
Db 19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy 61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
Db 79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy 121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
Db 139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy 181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
Db 199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy 241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
Db 259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy 301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
Db 319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy 361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
Db 379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy 421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
Db 439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy 481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
Db 499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy 541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
Db 559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613

RESULT 5
AAB48095
ID AAB48095 standard; protein; 805 AA.
XX
AC AAB48095;
XX
DT 19-MAR-2001 (first entry)
XX
DE Human Zace2 protein.
XX
KW Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility;
KW zinc metallopeptidase; blood pressure; zinc protease; hypertension;
KW ventricular systolic dysfunction; renal impairment; heart failure;
KW scleroderma renal crisis; atherosclerosis; antiinflammatory; human;
KW antiarthritic; bradykinin inactivator.
XX
OS Homo sapiens.
XX
PN WO200070032-A1.
XX
PD 23-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-US011932.
XX
PR 13-MAY-1999; 99US-00311482.
PR 27-AUG-1999; 99US-00384706.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Piddington CS, Petrie CR, Shoemaker KE, Bishop PD;
XX
DR WPI; 2001-025018/03.
DR N-PSDB; AAC84366, AAC84367.
XX
PT Angiotensin-converting enzyme, Zace2, useful for treating inflammatory
PT bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases
PT associated with inflammation such as arthritis and enterocolitis.
XX
PS Example 1; Page 95-100; 125pp; English.
XX
CC The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-
CC converting enzyme is a zinc metallopeptidase that plays roles in blood
CC pressure regulation and fertility. Zace2 can be expressed by standard
CC recombinant methodology. Zace2 polypeptides are useful for treating an
CC inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis),
CC diseases associated with inflammation like arthritis and enterocolitis,
CC as targets for identifying modulators of zinc protease activity, for
CC screening or identifying new angiotensin-converting enzyme (ACE)
CC inhibitors, and as a basis for rational drug design for inhibitory
CC molecules. The nucleic acids can be used to detect the expression of a
CC Zace2 gene in a biological sample, as probes for in vivo diagnosis and
CC for detecting and localizing Zace2 gene expression in tissue samples, to
CC determine whether a subject's chromosomes contain a mutation in the Zace2
CC gene, and to detect aberrations associated with the Zace2 locus.
CC Inhibitors of ACE are used for treating hypertension of various
CC conditions, including left ventricular systolic dysfunction, progressive
CC renal impairment, scleroderma renal crisis, congestive heart failure due
CC to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be
CC used to treat infertility while Zace2 antagonists are used for inducing
CC infertility. The present sequence represents the human Zace2 protein
XX
SQ Sequence 805 AA;

Query Match 100.0%; Score 3231; DB 4; Length 805;
Best Local Similarity 100.0%; Pred. No. 6.1e-288;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
Db 19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy 61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
Db 79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy 121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
Db 139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy 181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
Db 199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy 241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
Db 259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy 301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
```

```
RESULT 6
AAY72667
ID   AAY72667 standard; protein; 805 AA.
XX
AC   AAY72667;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Human angiotensin converting enzyme-2 (ACE-2).
XX
KW   Human; angiotensin converting enzyme-2; ACE-2; peptidyl dipeptidase A;
KW   screening; therapy; hypertension; congestive heart failure; CHF;
KW   inflammation; pain.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .18
FT                   /label= Signal_peptide
FT   Protein         19. .805
FT                   /label= Mature_ACE-2_protein
FT   Domain          374. .378
FT                   /label= ZBD
FT                   /note= "Zinc binding domain"
FT   Domain          741. .765
FT                   /label= TMD
FT                   /note= "Transmembrane domain; Hydrophobic region"
FT   Domain          766. .805
FT                   /label= Cytoplasmic_domain
XX
PN   US6194556-B1.
XX
PD   27-FEB-2001.
XX
PF   11-DEC-1997;   97US-00989299.
XX
PR   11-DEC-1997;   97US-00989299.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Acton SL,  Robison KE;
XX
DR   WPI; 2001-210604/21.
DR   N-PSDB; AAD02758.
XX
PT   Novel genes encoding angiotensin converting enzyme-2 useful as antisense
PT   or antigene agents for therapeutics, diagnostics and screening assays.
XX
PS   Claim 33; Fig 1; 76pp; English.
XX
CC   The present amino acid sequence is human angiotensin converting enzyme-2
CC   (ACE-2), also referred as peptidyl dipeptidase A (EC 3.4.15.1). Nucleic
CC   acid sequence encoding ACE-2 is useful as antisense or antigene agents
CC   for sequence specific modulation of gene expression or in the analysis of
CC   single base-pair mutations in the gene. Nucleic acid sequence encoding
CC   ACE-2 is useful in therapeutics, diagnostics and in screening assays. ACE
CC   -2 antagonist is used to treat hypertension or congestive heart failure
CC   (CHF). ACE agonist is used to reduce the inflammation and pain resulting
CC   from an insect sting or bite, which was accompanied by an injection of
CC   bradykinin. Anti-ACE-2 antibodies are used to monitor ACE-2 protein
CC   levels for determining the disease or condition associated with an
CC   aberrant protein level
XX
SQ   Sequence 805 AA;

  Query Match           100.0%;  Score 3231;  DB 4;  Length 805;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-288;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
```

```
RESULT 7
AAE20353
ID   AAE20353 standard; protein; 805 AA.
XX
AC   AAE20353;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human ACE-2 full-length protein.
XX
KW   Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
KW   peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
KW   myocardial infarction; heart failure; arrhythmia; renal failure; gene;
KW   inflammation; fertility; enzyme; EC 3.4.15.1.
XX
OS   Homo sapiens.
```

```
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .18
FT                   /label= Signal_peptide
FT   Protein         19. .805
FT                   /note= "Mature ACE-2 protein"
FT   Domain          19. .740
FT                   /note= "Extracellular domain"
FT   Domain          374. .378
FT                   /note= "Zinc binding domain (ZBD)"
FT   Domain          741. .765
FT                   /note= "Transmembrane domain"
FT   Domain          766. .805
FT                   /note= "Cytoplasmic domain"
XX
PN   WO200212471-A2.
XX
PD   14-FEB-2002.
XX
PF   09-AUG-2001; 2001WO-US025059.
XX
PR   09-AUG-2000; 2000US-00635501.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Acton S,  Robison KE,  Hsieh FY;
XX
DR   WPI; 2002-257481/30.
DR   N-PSDB; AAD32586.
XX
PT   Isolated human polypeptide, known as angiotensin converting enzyme-2,
PT   useful for treating or preventing the development of an abnormal blood
PT   pressure or related diseases, e.g. hypertension, heart failure or
PT   myocardial infarction.
XX
PS   Claim 2; Fig 1; 218pp; English.
XX
CC   The invention relates to human angiotensin converting enzyme-2 (ACE-2)
CC   polypeptides and polynucleotides. ACE-2 is also known as peptidyl
CC   dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
CC   treating or preventing the development of abnormal blood pressure and
CC   diseases or disorders associated with the protein in a subject. The
CC   diseases include hypertension, hypotension, congestive heart failure,
CC   chronic heart failure, acute heart failure, myocardial infarction,
CC   atherosclerosis, arrhythmia and renal failure. They are also useful for
CC   treating inflammatory conditions and diseases relating to fertility. The
CC   present sequence is human full-length ACE-2 protein
XX
SQ   Sequence 805 AA;

  Query Match             100.0%;  Score 3231;  DB 5;  Length 805;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-288;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613


RESULT 8
ABG77011
ID   ABG77011 standard; protein; 805 AA.
XX
AC   ABG77011;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Human angiotensin converting enzyme 2.
XX
KW   Aminopeptidase P; XPNEP2; bradykinin receptor B1; BDKRB1;
KW   tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;
KW   KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
KW   angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
KW   polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KW   cardiovascular disease; angina pectoris; hypertension; heart failure;
KW   myocardial infarction; ventricular hypertrophy; vascular disease;
KW   aneurysm; embolism; thrombosis; coronary artery disease; angioedaema;
KW   arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
KW   autoimmune disease; inflammatory arthritis; cancer; wound;
KW   viral infection; bacterial infection; fungal infection; COPD;
KW   Chronic obstructive pulmonary disease; enterocolitis.
XX
OS   Homo sapiens.
XX
PN   WO200261131-A2.
XX
PD   08-AUG-2002.
XX
PF   03-DEC-2001; 2001WO-US047235.
XX
PR   04-DEC-2000; 2000US-0251015P.
PR   23-JAN-2001; 2001US-0263678P.
PR   02-MAR-2001; 2001US-0273037P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA   (TSUC/) TSUCHIHASHI Z.
PA   (HUIL/) HUI L.
XX
PI   Tsuchihashi Z,  Hui L,  Zerba KE,  Ma-Edmonds M,  Perrone MH;
PI   Swanson BN,  Powell JR;
XX
DR   WPI; 2002-619265/66.
DR   N-PSDB; ABS60372.
XX
PT   New isolated nucleic acid with at least one polymorphic position, useful
PT   for detecting, diagnosing and treating disorders such as angioedema,
PT   cancer, viral, bacterial or fungal infection, cardiovascular and
PT   autoimmune diseases.
XX
PS   Disclosure; Fig 32; 977pp; English.
```

```
XX
CC   The invention relates to an isolated nucleic acid from a human gene
CC   encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1),
CC   tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
CC   1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
CC   2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
CC   polymorphic position. Also included are (1) a probe that hybridises to a
CC   polymorphic position as provided in the detailed summary of single
CC   nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC   sequence; (2) analysing (M1) at least one nucleic acid sample comprising
CC   obtaining the sample from one or more individuals and determining the
CC   nucleic acid sequence at one or more polymorphic positions in a gene
CC   encoding a protein selected from the group above; (3) constructing (M2)
CC   haplotypes using the genes comprising grouping at least two nucleic acids
CC   ; (4) identifying (M3) an individual at risk of developing a disorder
CC   upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
CC   using the polymorphic data; (5) a library of nucleic acids, each of which
CC   comprises one or more polymorphic positions within a gene encoding a
CC   human protein selected from the group above; and (6) genotyping (M4) an
CC   individual comprising obtaining a nucleic acid sample, determining the
CC   nucleotide present in at least one polymorphic position, and comparing at
CC   least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC   and compositions are useful for detecting, diagnosing, treating,
CC   preventing various disorders such as angioedaema and diseases which
CC   involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC   disease, trachomas, and cardiovascular diseases like angina pectoris,
CC   hypertension, heart failure, myocardial infarction, ventricular
CC   hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC   artery disease, arteriosclerosis and/or atherosclerosis, and
CC   hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC   arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC   obstructive pulmonary disease (COPD) and enterocolitis (many other
CC   diseases and disorders are listed in the specification). The
CC   polynucleotides are also useful for chromosome identification. Antibodies
CC   against the proteins may be utilised for immunophenotyping of cell lines
CC   and biological samples. The present sequence represents one of the
CC   proteins listed above
XX
SQ   Sequence 805 AA;

  Query Match             100.0%;  Score 3231;  DB 5;  Length 805;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-288;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613


RESULT 9
ABG77023
ID   ABG77023 standard; protein; 805 AA.
XX
AC   ABG77023;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Human angiotensin converting enzyme 2 variant #1.
XX
KW   Aminopeptidase P; XPNEP2; bradykinin receptor B1; human; BDKRB1;
KW   tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;
KW   KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
KW   angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
KW   polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KW   cardiovascular disease; angina pectoris; hypertension; heart failure;
KW   myocardial infarction; ventricular hypertrophy; vascular disease;
KW   aneurysm; embolism; thrombosis; coronary artery disease; angioedaema;
KW   arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
KW   autoimmune disease; inflammatory arthritis; cancer; wound;
KW   viral infection; bacterial infection; fungal infection; COPD;
KW   Chronic obstructive pulmonary disease; enterocolitis.
XX
OS   Homo sapiens.
XX
PN   WO200261131-A2.
XX
PD   08-AUG-2002.
XX
PF   03-DEC-2001; 2001WO-US047235.
XX
PR   04-DEC-2000; 2000US-0251015P.
PR   23-JAN-2001; 2001US-0263678P.
PR   02-MAR-2001; 2001US-0273037P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA   (TSUC/) TSUCHIHASHI Z.
PA   (HUIL/) HUI L.
XX
PI   Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
PI   Swanson BN, Powell JR;
XX
DR   WPI; 2002-619265/66.
DR   N-PSDB; ABS60633.
XX
PT   New isolated nucleic acid with at least one polymorphic position, useful
PT   for detecting, diagnosing and treating disorders such as angioedema,
PT   cancer, viral, bacterial or fungal infection, cardiovascular and
PT   autoimmune diseases.
XX
PS   Disclosure; Fig 37; 977pp; English.
XX
CC   The invention relates to an isolated nucleic acid from a human gene
CC   encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1),
CC   tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
CC   1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
CC   2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
CC   polymorphic position. Also included are (1) a probe that hybridises to a
CC   polymorphic position as provided in the detailed summary of single
CC   nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC   sequence; (2) analysing (M1) at least one nucleic acid sample comprising
```

```
CC   obtaining the sample from one or more individuals and determining the
CC   nucleic acid sequence at one or more polymorphic positions in a gene
CC   encoding a protein selected from the group above; (3) constructing (M2)
CC   haplotypes using the genes comprising grouping at least two nucleic acids
CC   ; (4) identifying (M3) an individual at risk of developing a disorder
CC   upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
CC   using the polymorphic data; (5) a library of nucleic acids, each of which
CC   comprises one or more polymorphic positions within a gene encoding a
CC   human protein selected from the group above; and (6) genotyping (M4) an
CC   individual comprising obtaining a nucleic acid sample, determining the
CC   nucleotide present in at least one polymorphic position, and comparing at
CC   least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC   and compositions are useful for detecting, diagnosing, treating,
CC   preventing various disorders such as angioedaema and diseases which
CC   involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC   disease, trachomas, and cardiovascular diseases like angina pectoris,
CC   hypertension, heart failure, myocardial infarction, ventricular
CC   hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC   artery disease, arteriosclerosis and/or atherosclerosis, and
CC   hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC   arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC   obstructive pulmonary disease (COPD) and enterocolitis (many other
CC   diseases and disorders are listed in the specification). The
CC   polynucleotides are also useful for chromosome identification. Antibodies
CC   against the proteins may be utilised for immunophenotyping of cell lines
CC   and biological samples. The present sequence represents a polymorphic
CC   variant of one of the proteins listed above
XX
SQ   Sequence 805 AA;

  Query Match             100.0%;  Score 3231;  DB 5;  Length 805;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-288;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
```

```
RESULT 10
AAU99701
ID   AAU99701 standard; protein; 805 AA.
XX
AC   AAU99701;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Human angiotensin converting enzyme-2 (ACE-2) protein.
XX
KW   Human; angiotensin converting enzyme-2; ACE-2; body weight disorder;
KW   muscle mass; body fat; obesity; diabetes; atherosclerosis; weight loss;
KW   lipid metabolism; weight gain; anorexia; cachexia; bulimia; sepsis;
KW   familial partial lipodystrophy; hypercholesterolaemia; hyperlipidaemia;
KW   aberrant metabolic rate; heart failure; left ventricular hypertrophy;
KW   neurodegenerative disorder; peptide hormone; cytokine processing;
KW   myocardial infarction; cardiomyopathy; inflammatory bowel disease;
KW   systemic inflammation response syndrome; polytrauma; pain; stroke;
KW   bone destruction; rheumatoid arthritis; osteoarthritis; asthma;
KW   periodontal disease; dysmenorrhoea; premature labour; brain oedema;
KW   focal injury; diffuse axonal injury; reperfusion injury; scar formation;
KW   cerebral vasospasm; subarachnoid haemorrhage; allergic disorder;
KW   adult respiratory distress syndrome; wound healing; appetite;
KW   body mass index.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .18
FT                   /label= Signal_peptide
FT   Protein         19. .805
FT                   /label= Mature_human_ACE_2_protein
XX
PN   WO200239997-A2.
XX
PD   23-MAY-2002.
XX
PF   31-OCT-2001; 2001WO-US045703.
XX
PR   01-NOV-2000; 2000US-00704216.
PR   29-MAY-2001; 2001US-00870382.
PR   19-OCT-2001; 2001US-0371741P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Acton SL,  Ocain TD,  Gould AE,  Dales NA,  Guan B,  Brown JA;
PI   Patane M,  Kadambi VJ,  Solomon M,  Stricker-Krongrad A;
XX
DR   WPI; 2002-547572/58.
DR   N-PSDB; ABK87623.
XX
PT   Treating body weight disorder and increasing muscle mass comprises
PT   administering angiotensin converting enzyme-2 modulating compound.
XX
PS   Example 5; Page 387-390; 395pp; English.
XX
CC   The present invention describes a new method of treating a body weight
CC   disorder, increasing muscle mass and decreasing body fat by
CC   administration of angiotensin converting enzyme (ACE)-2 modulating
CC   compound. The invention can be used for treating body weight disorders,
CC   particularly obesity of at least grade 1, diabetes, atherosclerosis and a
CC   state associated with lipid metabolism. The method is used for treating
CC   rapid weight loss, rapid weight gain, anorexia, cachexia, bulimia,
CC   generalised partial lipodystrophy, familial partial lipodystrophy,
CC   hypercholesterolaemia, hyperlipidaemia, an aberrant metabolic rate,
CC   congestive heart failure, chronic heart failure, left ventricular
CC   hypertrophy, acute heart failure, neurodegenerative disorders (e.g.
CC   Alzheimer's disease, Parkinson's disease and Huntington's disease),
CC   diseases associated with peptide hormones or cytokine processing,
CC   myocardial infarction, cardiomyopathy, systemic inflammation response
CC   syndrome, sepsis, polytrauma, inflammatory bowel disease, acute and
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CC   chronic pain, bone destruction in rheumatoid arthritis and osteoarthritis
CC   and periodontal disease, dysmenorrhoea, premature labour, brain oedema
CC   following focal injury, diffuse axonal injury, stroke, reperfusion
CC   injury, cerebral vasospasm after subarachnoid haemorrhage, allergic
CC   disorders including asthma, adult respiratory distress syndrome, wound
CC   healing and scar formation. The invention decreases the appetite,
CC   increases muscle mass and decreases body fat of subject having body mass
CC   index of greater than 23 (preferably 24.9)kg/m^2. The present amino acid
CC   sequence represents the human ACE-2 protein of the invention
XX
SQ   Sequence 805 AA;

  Query Match             100.0%;  Score 3231;  DB 5;  Length 805;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-288;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613


RESULT 11
ABU07731
ID   ABU07731 standard; protein; 805 AA.
XX
AC   ABU07731;
XX
DT   27-MAY-2003  (first entry)
XX
DE   Human zinc metallopeptidase Zace2.
XX
KW   Human; enzyme; Zace2; zinc metallopeptidase; ulcerative colitis;
KW   inflammation; inflammatory bowel disease; arthritis; enterocolitis;
KW   Crohn's disease; gene therapy; transgenic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          371. .380
FT                   /label= Expanded_zinc_binding_region
FT   Region          374. .378
FT                   /label= Zinc-binding_motif
FT   Domain          739. .761
FT                   /label= Transmembrane_domain
XX
PN   US2002177211-A1.
XX
PD   28-NOV-2002.
XX
PF   16-OCT-2001; 2001US-00978385.
XX
PR   13-MAY-1999;   99US-0133952P.
PR   27-AUG-1999;   99US-0151181P.
PR   03-MAY-2000; 2000US-00563516.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Piddington CS,  Petrie C,  Shoemaker KE,  Bishop PD;
XX
DR   WPI; 2003-328489/31.
DR   N-PSDB; ABX93333.
XX
PT   Isolated human or murine Zace2 polypeptide useful for reducing
PT   inflammation in conditions such as inflammatory bowel disease, arthritis,
PT   enterocolitis, ulcerative colitis and Crohn's disease.
XX
PS   Claim 1; Page 39-41; 57pp; English.
XX
CC   The invention relates to an isolated polypeptide, comprising fully
CC   defined human Zace2, murine Zace-5, or murine Zace2-10 polypeptide. An
CC   expression vector containing Zace2 polynucleotide is useful for producing
CC   Zace2 protein. The polynucleotide is useful as a diagnostic probe for
CC   detecting a product of Zace2 gene expression in a biological sample. The
CC   polypeptide is also useful for decreasing inflammation associated with a
CC   condition such as inflammatory bowel disease, arthritis or enterocolitis.
CC   The polypeptide is also useful for treating Crohn's disease and
CC   ulcerative colitis. The polypeptide is useful for producing labelled
CC   angiotensin II, for identifying modulators of zinc protease activity and
CC   for identifying angiotensin converting enzyme (ACE) inhibitors. The
CC   polynucleotide is useful in gene therapy techniques to treat the above
CC   mentioned disorders. The polynucleotide is also useful for determining
CC   whether a subject's chromosome contains a mutation in the Zace2 gene. The
CC   present sequence represents the amino acid sequence of human zinc
CC   metallopeptidase Zace2
XX
SQ   Sequence 805 AA;

  Query Match             100.0%;  Score 3231;  DB 6;  Length 805;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-288;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
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Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
```

RESULT 12
ADA03344
ID ADA03344 standard; protein; 805 AA.
XX
AC ADA03344;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human angiotensin converting enzyme 2-like protein.
XX
KW hypotensive; cardiant; cerebroprotective; antiatherosclerotic; analgesic;
KW antiinflammatory; nephrotropic; hypertensive; vasotropic; cytostatic;
KW antiasthmatic; antiallergic; neuroprotective; antiparkinsonian;
KW nootropic; antirheumatic; antiarthritic; antigout; tranquillizer;
KW vulnerary; antidiabetic; dermatological; immunosuppressive; hepatotropic;
KW anti-HIV; antibacterial; angiotensin converting enzyme; ACE-2;
KW angiotensin converting enzyme; ACE-2; hypertension;
KW congestive heart failure; stroke; left ventricular failure;
KW atherosclerotic heart disease; stenosis; pain; inflammatory reaction;
KW histamine; vasoconstriction; epitope; aldosterone; cell proliferation;
KW renal disorder; acute glomerulonephritis; immunophenotyping;
KW cardiac myocyte; Bowman's capsule; hypotensin; ischemia; asthma; allergy;
KW multiple sclerosis; cancer; Parkinson's disease; Alzheimer's disease;
KW rheumatoid arthritis; gout; trauma; dermatitis; diabetes mellitus;
KW Sjogren's syndrome; Addison's disease; hepatitis; Crohn's disease;
KW sarcoidosis; AIDS; sepsis.
XX
OS Homo sapiens.
XX
PN WO200298448-A1.
XX
PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017199.
XX
PR 04-JUN-2001; 2001US-0294976P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Parry TJ, Rosen CA, Albert VR, Sanyal I, Huang L, Wescott CR;
PI Sekut L;
XX
DR WPI; 2003-140552/13.
DR N-PSDB; ADA03343.
XX
PT Novel angiotensin converting enzyme-2 binding polypeptide useful for
PT treating, preventing or ameliorating hypertension, congestive heart
PT failure, stroke, left ventricular failure and atherosclerotic heart
PT disease.
XX
PS Disclosure; Page 239-241; 246pp; English.
XX
CC The invention relates to novel isolated angiotensin converting enzyme
CC (ACE)-2 binding polypeptides (I), which are useful for treating,
CC preventing or ameliorating hypertension, congestive heart failure,
CC stroke, left ventricular failure and atherosclerotic heart disease in an
CC animal. The peptides are useful for detecting, isolating, or purifying
CC ACE-2 proteins or ACE-2 like polypeptides in solutions, mixtures, or
CC biological samples; for inhibiting or reducing stenosis, pain,
CC inflammatory reactions, abnormal histamine release, vasoconstriction,
CC diseases or disorders related to vasoconstriction, and diseases and/or
CC disorders associated with aberrant action of ACE-2; to detect, isolate,
CC or remove ACE-2 target proteins in solutions, and also to identify
CC epitopes of ACE-2; to detect, diagnose, prognose, or monitor
CC cardiovascular diseases, and disorders associated with aberrant
CC aldosterone activity, or cell proliferation; for preventing and treating
CC renal disorders, e.g., acute glomerulonephritis, and diseases associated
CC with it; to assay protein levels in a biological sample, for
CC immunophenotyping of cell lines and biological samples by their ACE-2
CC expression, and for identifying cells, such as cardiac myocytes,
CC endothelial and epithelial cells of Bowman's capsule. The peptides are
CC especially useful for treating, preventing, or ameliorating diseases or
CC disorders associated with hypotensin, ischemia, asthma, allergy, multiple
CC sclerosis, cancers, Parkinson's and Alzheimer's diseases, rheumatoid
CC arthritis, gout, trauma, dermatitis, diabetes mellitus, Sjogren's
CC syndrome, Addison's disease, chronic active hepatitis, Crohn's disease,
CC sarcoidosis, AIDS, and sepsis. In an example of the invention, ACE-2
CC binding peptides were isolated from a number of peptide display
CC libraries. Evaluation of the peptide sequences revealed a series of
CC peptide families. This sequence represents a human angiotensin converting
CC enzyme 2-like protein.
XX
SQ Sequence 805 AA;

Query Match 100.0%; Score 3231; DB 6; Length 805;
Best Local Similarity 100.0%; Pred. No. 6.1e-288;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558
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Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
```

RESULT 13
ABR56712
ID ABR56712 standard; protein; 805 AA.
XX
AC ABR56712;
XX
DT 30-JUL-2003 (first entry)
XX
DE Human ACE-2 protein SEQ ID NO:142.
XX
KW Human; angiotensin converting enzyme 2; ACE-2 binding; ACE-2;
KW vasoconstriction; low blood pressure; angiotensin II; angiotensin;
KW hypertensive; vasotropic; vaccine; hypotension; shock; syncope.
XX
OS Homo sapiens.
XX
PN WO200298906-A1.
XX
PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017213.
XX
PR 04-JUN-2001; 2001US-0295004P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Parry TJ;
XX
DR WPI; 2003-140586/13.
DR N-PSDB; ACC79022.
XX
PT Increasing vasoconstriction or ameliorating a disorder resulting from low
PT blood pressure, e.g. hypotension, shock or syncope, comprises
PT administering an angiotensin II in combination with angiotensin 1-9 to an
PT individual.
XX
PS Disclosure; Page 227-229; 237pp; English.
XX
CC The present invention describes a method for increasing vasoconstriction
CC or ameliorating a disorder resulting from low blood pressure, which
CC comprises administering to an individual an amount of angiotensin II in
CC combination with angiotensin 1-9. Angiotensin has hypertensive and
CC vasotropic activities, and can be used in vaccines. The method is useful
CC for increasing vasoconstriction or ameliorating a disorder resulting from
CC low blood pressure, such as hypotension, shock or syncope. ABR56563 to
CC ABR56708 represent angiotensin converting enzyme 2 (ACE-2) binding
CC peptides, ABR56709 to ABR56725 and ACC79021 to ACC79025 represent
CC sequences used in the exemplification of the present invention. Human ACE
CC -2 is located to chromosome X, more specifically to Xp22. N.B. ABR56563
CC to ABR56572 represent SEQ ID NO:1 to 10 and should be the same as
CC ABR56573 to ABR56582, but the Z's given at the beginning and end of the
CC peptides in the disclosure have been expanded to Glx in the Sequence
CC Listing and in this case the Z's do not represent Gln or Glu (see pages 4
CC to 7). SEQ ID NO:40 to 136 in the Sequence Listing (see also pages 7 to
CC 10) have been specified as SEQ ID NO:20 to 116 in Example 1 (see pages
CC 174 to 177)
XX
SQ Sequence 805 AA;

Query Match 100.0%; Score 3231; DB 6; Length 805;
Best Local Similarity 100.0%; Pred. No. 6.1e-288;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
```

RESULT 14
ADL95395
ID ADL95395 standard; protein; 805 AA.
XX
AC ADL95395;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human angiotensin converting enzyme-2 (ACE-2).
XX
KW bioactivity; angiotensin converting enzyme-2; ACE-2; human; enzyme;
KW carboxypeptidase.
XX
OS Homo sapiens.
XX
PN US6610497-B1.
XX
PD 26-AUG-2003.
XX
PF 29-SEP-1999; 99US-00407427.
XX
PR 11-DEC-1997; 97US-00989299.
PR 30-SEP-1998; 98US-00163648.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Acton SL, Robison KE, Hsieh FY;
XX
DR WPI; 2003-895335/82.
DR N-PSDB; ADL95394, ADL95396.
XX
PT Identification of compound that modulates bioactivity of angiotensin
PT converting enzymes-2 polypeptide, by detecting modulation of the
PT bioactivity of polypeptide that is contacted with test compound as
PT compared to control.
XX
PS Claim 6; SEQ ID NO 2; 91pp; English.

```
XX
CC   The invention describes a compound that modulates bioactivity of an
CC   angiotensin converting enzyme-2 (ACE-2) polypeptide. The compound is
CC   identified by contacting an ACE-2 polypeptide with a test compound under
CC   conditions for modulation of the bioactivity of the polypeptide; and
CC   detecting modulation of the bioactivity of the polypeptide by the test
CC   compound as compared to a control. Also described is a method for
CC   modulating the bioactivity of an ACE-2 polypeptide by contacting the ACE-
CC   2 polypeptide with a compound that has been identified. The method is
CC   useful for identifying a compound that modulates the bioactivity of
CC   angiotensin converting enzyme-2 peptides. The inventive method identifies
CC   other potential substrates of ACE-2 polypeptides and the product of the
CC   enzymatic reaction. The comparison of the mass spectra of the test
CC   compound with that of the reaction mixture after incubation indicates
CC   whether the test compound was converted into a new compound, in which
CC   case the test compound is a substrate of the ACE-2 polypeptide. This is
CC   the amino acid sequence of human angiotensin converting enzyme-2 (ACE-2).
XX
SQ   Sequence 805 AA;

  Query Match             100.0%;  Score 3231;  DB 7;  Length 805;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-288;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613


RESULT 15
ADL95494
ID   ADL95494 standard; protein; 805 AA.
XX
AC   ADL95494;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human angiotensin converting enzyme-2 (ACE-2) N720D.
XX
KW   bioactivity; angiotensin converting enzyme-2; ACE-2; human; enzyme;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 720
FT                   /note= "Wild type Asn substituted by Asp"
XX
PN   US6610497-B1.
XX
PD   26-AUG-2003.
XX
PF   29-SEP-1999;   99US-00407427.
XX
PR   11-DEC-1997;   97US-00989299.
PR   30-SEP-1998;   98US-00163648.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Acton SL,  Robison KE,  Hsieh FY;
XX
DR   WPI; 2003-895335/82.
DR   N-PSDB; ADL95394.
XX
PT   Identification of compound that modulates bioactivity of angiotensin
PT   converting enzymes-2 polypeptide, by detecting modulation of the
PT   bioactivity of polypeptide that is contacted with test compound as
PT   compared to control.
XX
PS   Disclosure; SEQ ID NO 100; 91pp; English.
XX
CC   The invention describes a compound that modulates bioactivity of an
CC   angiotensin converting enzyme-2 (ACE-2) polypeptide. The compound is
CC   identified by contacting an ACE-2 polypeptide with a test compound under
CC   conditions for modulation of the bioactivity of the polypeptide; and
CC   detecting modulation of the bioactivity of the polypeptide by the test
CC   compound as compared to a control. Also described is a method for
CC   modulating the bioactivity of an ACE-2 polypeptide by contacting the ACE-
CC   2 polypeptide with a compound that has been identified. The method is
CC   useful for identifying a compound that modulates the bioactivity of
CC   angiotensin converting enzyme-2 peptides. The inventive method identifies
CC   other potential substrates of ACE-2 polypeptides and the product of the
CC   enzymatic reaction. The comparison of the mass spectra of the test
CC   compound with that of the reaction mixture after incubation indicates
CC   whether the test compound was converted into a new compound, in which
CC   case the test compound is a substrate of the ACE-2 polypeptide. This is
CC   the amino acid sequence of human angiotensin converting enzyme-2 (ACE-2)
CC   N720D mutant. Note: This sequence does not appear in the printed
CC   specification but has been created by the indexer using information given
CC   in the invention.
XX
SQ   Sequence 805 AA;

  Query Match             100.0%;  Score 3231;  DB 7;  Length 805;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-288;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198
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Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
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Search completed: March 28, 2006, 11:09:51
Job time : 137.885 secs

GenCore version 5.1.7


OM protein - protein search, using sw model

Run on: March 28, 2006, 11:10:19 ; Search time 21.8626 Seconds
(without alignments)
2618.576 Million cell updates/sec

Title: US-10-659-000-4
Perfect score: 3231
Sequence: 1 STIEEQAKTFLDKFNHEAED.....WLKDQNKNSFVGWSTDWSPY 595

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 3231 | 100.0 | 804 | 2 | T14762 | hypothetical prote |
| 2 | 1335 | 41.3 | 732 | 1 | S05238 | peptidyl-dipeptida |
| 3 | 1335 | 41.3 | 1306 | 1 | A31759 | peptidyl-dipeptida |
| 4 | 1334 | 41.3 | 732 | 1 | A35655 | peptidyl-dipeptida |
| 5 | 1334 | 41.3 | 1312 | 1 | A34171 | peptidyl-dipeptida |
| 6 | 1310 | 40.5 | 1313 | 1 | JC2038 | peptidyl-dipeptida |
| 7 | 1307 | 40.5 | 1193 | 2 | JC2489 | peptidyl-dipeptida |
| 8 | 1281 | 39.6 | 737 | 1 | A34402 | peptidyl-dipeptida |
| 9 | 1281 | 39.6 | 1309 | 1 | S35484 | peptidyl-dipeptida |
| 10 | 1054.5 | 32.6 | 611 | 2 | S65472 | peptidyl-dipeptida |
| 11 | 1027.5 | 31.8 | 630 | 2 | JC5374 | angiotensin-conver |
| 12 | 1022 | 31.6 | 615 | 2 | A57533 | peptidyl-dipeptida |
| 13 | 635.5 | 19.7 | 907 | 2 | T15792 | hypothetical prote |
| 14 | 157 | 4.9 | 532 | 2 | C83696 | hypothetical prote |
| 15 | 154 | 4.8 | 502 | 2 | AF1310 | probable thermosta |
| 16 | 147 | 4.5 | 502 | 2 | AE1682 | probable thermosta |
| 17 | 139.5 | 4.3 | 987 | 2 | AI2011 | peptide synthetase |
| 18 | 139 | 4.3 | 608 | 2 | B82938 | zinc metalloprotei |
| 19 | 136 | 4.2 | 611 | 2 | D82881 | zinc metalloprotei |
| 20 | 135 | 4.2 | 501 | 2 | D69943 | carboxypeptidase h |
| 21 | 124 | 3.8 | 538 | 2 | E72561 | probable thermosta |
| 22 | 121 | 3.7 | 607 | 2 | AB3511 | oligoendopeptidase |
| 23 | 121 | 3.7 | 1034 | 2 | T30574 | beta-galactosidase |
| 24 | 118 | 3.7 | 627 | 1 | S40048 | 1,4-alpha-glucan b |
| 25 | 117.5 | 3.6 | 987 | 2 | I48373 | G-utrophin - mouse |
| 26 | 115.5 | 3.6 | 611 | 2 | A75573 | probable oligoendo |
| 27 | 114 | 3.5 | 685 | 2 | F75370 | oligopeptidase A - |
| 28 | 113.5 | 3.5 | 3655 | 2 | T38084 | TRAP-like protein |
| 29 | 113 | 3.5 | 772 | 2 | AI0968 | probable glycosyl |
| 30 | 112 | 3.5 | 524 | 2 | B82202 | thermostable carbo |
| 31 | 111.5 | 3.5 | 282 | 2 | H97226 | protein containing |
| 32 | 110.5 | 3.4 | 4540 | 2 | T30838 | cytoplasmic dynein |
| 33 | 110 | 3.4 | 499 | 2 | AG0281 | probable carboxype |
| 34 | 110 | 3.4 | 1034 | 2 | T30551 | beta-galactosidase |
| 35 | 110 | 3.4 | 1642 | 2 | T08880 | NMDA receptor-bind |
| 36 | 109.5 | 3.4 | 642 | 2 | E98000 | 1,4-alpha-glucan b |
| 37 | 109 | 3.4 | 990 | 2 | S23416 | lantibiotic epider |
| 38 | 108.5 | 3.4 | 1339 | 2 | A84683 | probable SNF2 subf |
| 39 | 108.5 | 3.4 | 3433 | 1 | S28381 | utrophin - human |
| 40 | 107.5 | 3.3 | 642 | 2 | G95129 | 1,4-alpha-glucan b |
| 41 | 107.5 | 3.3 | 710 | 2 | AG2285 | hypothetical prote |
| 42 | 107.5 | 3.3 | 819 | 2 | T29486 | hypothetical prote |
| 43 | 107.5 | 3.3 | 1397 | 2 | T51292 | Dna2p - fission ye |
| 44 | 107.5 | 3.3 | 1398 | 2 | T39568 | hypothetical helic |
| 45 | 107 | 3.3 | 736 | 1 | VPXRPC | outer layer protei |

ALIGNMENTS

RESULT 1
T14762
hypothetical protein DKFZp434A014.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14762
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, August 1999
A;Reference number: Z18181
A;Accession: T14762
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-804 <WAM>
A;Cross-references: UNIPROT:Q9UFZ6; UNIPARC:UPI000006FF2B; EMBL:AL110224
A;Experimental source: adult testis; clone DKFZp434A014
C;Genetics:
A;Note: DKFZp434A014.1

Query Match 100.0%; Score 3231; DB 2; Length 804;
Best Local Similarity 100.0%; Pred. No. 3.6e-224;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 77

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 137

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 197

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 257

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 317

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 377

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 437

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        438 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 497

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 557

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 612


RESULT 2
S05238
peptidyl-dipeptidase A (EC 3.4.15.1) precursor, testicular splice form - human
N;Alternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxypepti
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: S05238; A33979
R;Lattion, A.L.; Soubrier, F.; Allegrini, J.; Hubert, C.; Corvol, P.; Alhenc-Gelas, F.
FEBS Lett. 252, 99-104, 1989
A;Title: The testicular transcript of the angiotensin I-converting enzyme encodes for th
A;Reference number: S05238; MUID:89338720; PMID:2547653
A;Accession: S05238
A;Molecule type: mRNA
A;Residues: 1-732 <LAT>
A;Cross-references: UNIPROT:P22966; UNIPARC:UPI000002DB19; EMBL:X16295; NID:g28264; PIDN
R;Ehlers, M.R.W.; Fox, E.A.; Strydom, D.J.; Riordan, J.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 7741-7745, 1989
A;Title: Molecular cloning of human testicular angiotensin-converting enzyme: the testis
A;Reference number: A33979; MUID:90046671; PMID:2554286
A;Accession: A33979
A;Molecule type: mRNA
A;Residues: 1-732 <EHL>
A;Cross-references: UNIPARC:UPI000002DB19; GB:M26657; NID:g338666; PIDN:AAA60611.1; PID:
A;Experimental source: clones R1.2 and T8B
A;Note: neither the complete nucleic acid sequence nor the complete translation are show
C;Comment: For the renal and pulmonary splice form, see PIR:A31759.
C;Genetics:
A;Gene: GDB:DCP1; ACE
A;Cross-references: GDB:119840; OMIM:106180
A;Map position: 17q23-17q23
C;Function:
A;Description: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypepti
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: alternative splicing; glycoprotein; metalloproteinase; peptidyldipeptide hyd
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-732/Product: peptidyl dipeptidase I #status predicted <MAT>
F;686-702/Domain: transmembrane #status predicted <TRM>
F;103,121,140,186,368,617,651/Binding site: carbohydrate (Asn) (covalent) #status predic
F;414,418,434/Binding site: zinc, catalytic (His, His, Glu) #status predicted
F;415/Active site: Glu #status predicted

  Query Match             41.3%;  Score 1335;  DB 1;  Length 732;
  Best Local Similarity   41.9%;  Pred. No. 6.6e-88;
  Matches  254;  Conservative  116;  Mismatches  202;  Indels   34;  Gaps    9;

Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE--------NVQNMNNAGDKWSA 53
              | | :|  |:::::  :: :: : : |:|||||||| |         |:|  |:
Db         70 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT------ 123

Qy         54 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 113
                 :  | |: : : ::|| |:|  :: :|    : |   : :  | ||  | | ||
Db        124 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 181

Qy        114 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 173
              ||:|:    || ||| |  :|| |  | : ||||| || : |: :   | :|| | |: |
Db        182 VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 239

Qy        174 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 233
              | | | | || ||  ||   ::          :|:|  |:|::||| :||||||  |
Db        240 RLNGYVDAGDSWRSMYETPSLE----------QDLERLFQELQPLYLNLHAYVRRALHRH 289

Qy        234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 292
              |   :|:  | :||||||:|| : |:|:| | |||   |::| |:||: | |  :|:|||
Db        290 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 349

Qy        293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
              |: || |:||  :   ||  |||  | : :: ||| :|||   | ||||  || | ::|
Db        350 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 409

Qy        352 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
              : |||||||||| | |   |  || ||| |||||:|::::|| :|||||  |: ||| :
Db        410 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 469

Qy        412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
              | | :||||:| ||  :  :||:|::::||| || | | |: : ::|| :: :  |:
Db        470 SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 528

Qy        472 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 531
              |||  :   || : ||: :   :|||:   : |||| ||||||| | ||||||||  | |
Db        529 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 588

Qy        532 AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 588
              |||:|   ::|| | ||  |:: : |  ||:   :|:||:|| ||: :|:     :||
Db        589 AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 648

Qy        589 STDWSP 594
                :|:|
Db        649 QYNWTP 654


RESULT 3
A31759
peptidyl-dipeptidase A (EC 3.4.15.1) precursor, renal and pulmonary splice form - human
N;Alternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxypeptic
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: A31759; PQ0004
R;Soubrier, F.; Alhenc-Gelas, F.; Hubert, C.; Allegrini, J.; John, M.; Tregear, G.; Corvo
Proc. Natl. Acad. Sci. U.S.A. 85, 9386-9390, 1988
A;Title: Two putative active centers in human angiotensin I-converting enzyme revealed by
A;Reference number: A31759; MUID:89071703; PMID:2849100
A;Accession: A31759
A;Molecule type: mRNA
A;Residues: 1-1306 <SOU>
A;Cross-references: UNIPROT:P12821; UNIPARC:UPI000002B8AD; GB:J04144; NID:g178285; PIDN:A
A;Experimental source: kidney
A;Note: parts of this sequence, including the amino end of the mature protein, were deter
R;Takeuchi, K.; Shimizu, T.; Ohishi, N.; Seyama, Y.; Takaku, F.; Yotsumoto, H.
J. Biochem. 106, 442-445, 1989
A;Title: Purification of human lung angiotensin-converting enzyme by high-performance lic
A;Reference number: PQ0004; MUID:90110025; PMID:2558109
A;Accession: PQ0004
A;Molecule type: protein
A;Residues: 'XX',32-34,'E',36-37,'X',39-41,'R',43-46 <TAK>
A;Cross-references: UNIPARC:UPI0000172A3D
A;Experimental source: lung
C;Comment: This splice form is found in many tissues, in particular kidney and lung vascu
C;Genetics:
A;Gene: GDB:DCP1; ACE
A;Cross-references: GDB:119840; OMIM:106180
A;Map position: 17q23-17q23
C;Function:
A;Description: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypeptic
A;Note: plays a role in the control of blood pressure by catalyzing the conversion of ang
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: alternative splicing; blood pressure control; glycoprotein; kidney; lung; met
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-1306/Product: peptidyl dipeptidase I #status predicted <MAT>
F;1260-1276/Domain: transmembrane #status predicted <TRM>
F;38,54,74,111,146,160,318,445,509,523,677,695,714,760,942,1191,1225/Binding site: carbol
F;390,394/Binding site: zinc (His) #status predicted
F;988,992,1008/Binding site: zinc, catalytic (His, His, Glu) #status predicted
F;989/Active site: Glu #status predicted

  Query Match             41.3%;  Score 1335;  DB 1;  Length 1306;
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Best Local Similarity 41.9%; Pred. No. 1.6e-87;
Matches 254; Conservative 116; Mismatches 202; Indels 34; Gaps 9;

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Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE--------NVQNMNNAGDKWSA 53
Db        644 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT------ 697

Qy         54 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 113
Db        698 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 755

Qy        114 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 173
Db        756 VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 813

Qy        174 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 233
Db        814 RLNGYVDAGDSWRSMYETPSLE----------QDLERLFQELQPLYLNLHAYVRRALHRH 863

Qy        234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 292
Db        864 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 923

Qy        293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
Db        924 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 983

Qy        352 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
Db        984 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 1043

Qy        412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
Db       1044 SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 1102

Qy        472 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 531
Db       1103 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 1162

Qy        532 AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 588
Db       1163 AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 1222

Qy        589 STDWSP 594
Db       1223 QYNWTP 1228
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RESULT 4
A35655
peptidyl-dipeptidase A (EC 3.4.15.1), testis - mouse
N;Alternate names: peptidyl-dipeptidase I, testis
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A35655
R;Howard, T.E.; Shai, S.Y.; Langford, K.G.; Martin, B.M.; Bernstein, K.E.
Mol. Cell. Biol. 10, 4294-4302, 1990
A;Title: Transcription of testicular angiotensin-converting enzyme (ACE) is initiated wi
A;Reference number: A35655; MUID:90318396; PMID:2164636
A;Accession: A35655
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-732 <HOW>
A;Cross-references: UNIPROT:P22967; UNIPARC:UPI0000020BD5; GB:M55333; NID:g191589; PIDN:
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: alternative splicing; peptidyldipeptide hydrolase; transmembrane protein; zi

Query Match 41.3%; Score 1334; DB 1; Length 732;
Best Local Similarity 42.6%; Pred. No. 7.8e-88;
Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;

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Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 61
Db         69 TDEAKADRFVEEYDRTAQVLLNEYAEANWQYNTNITIEGSKILLEKSTEVSNHTLKYGTR 128

Qy         62 AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 121
Db        129 AKTFDVSNFQNSSIKRIIKKLQNLDRAVLPPKELEEYNQILLDMETTYSLSNICYTNG-- 186

Qy        122 ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 181
Db        187 TCMPLEPDLTNMMATSRKYEELLWAWKSWRDKVGRAILPFFPKYVEFSNKIAKLNGYTDA 246

Qy        182 GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 240
Db        247 GDSWRSLYESDNLE----------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 296

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
Db        297 DGPIPAHLLGNMWAQTWSNIYDLVAPFPSAPNIDATEAMIKQGWTPRRIFKEADNFFTSL 356

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG 359
Db        357 GLLPVPPEFWNKSMLEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMG 416

Qy        360 HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 419
Db        417 HIQYFMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN 475

Qy        420 FLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 479
Db        476 FLMKMALDKIAFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGD 535

Qy        480 CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM 539
Db        536 FDPGSKFHVPANVPYVRYFVSFIIQFQFHEALCRAAGHTGPLHKCDIYQSKEAGKLLADA 595

Qy        540 LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 594
Db        596 MKLGYSKPWPEAMKLITGQPNMSASAMMNYFKPLTEWLVTENRRHGETLGWPEYNWAP 653
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RESULT 5
A34171
peptidyl-dipeptidase A (EC 3.4.15.1) precursor - mouse
N;Alternate names: ACE; angiotensin-converting enzyme; carboxycathepsin; dipeptidyl carbo
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A34171; A29220; A61477
R;Bernstein, K.E.; Martin, B.M.; Edwards, A.S.; Bernstein, E.A.
J. Biol. Chem. 264, 11945-11951, 1989
A;Title: Mouse angiotensin-converting enzyme is a protein composed of two homologous doma
A;Reference number: A34171; MUID:89308599; PMID:2545691
A;Accession: A34171
A;Molecule type: mRNA
A;Residues: 1-1312 <BER>
A;Cross-references: UNIPROT:P09470; UNIPARC:UPI0000029F6E; GB:J04947
R;Bernstein, K.E.; Martin, B.M.; Bernstein, E.A.; Linton, J.; Striker, L.; Striker, G.
J. Biol. Chem. 263, 11021-11024, 1988
A;Title: The isolation of angiotensin-converting enzyme cDNA.
A;Reference number: A29220; MUID:88298730; PMID:2841312
A;Accession: A29220
A;Molecule type: mRNA
A;Residues: 1-332 <BE2>
A;Cross-references: UNIPARC:UPI000016CBC0; GB:J03940; NID:g191583; PIDN:AAA37146.1; PID:g
R;Bernstein, K.E.; Martin, B.M.; Striker, L.; Striker, G.
Kidney Int. 33, 652-655, 1988
A;Title: Partial protein sequence of mouse and bovine kidney angiotensin converting enzym
A;Reference number: A61477; MUID:88215372; PMID:2835538
A;Accession: A61477
A;Status: preliminary
A;Molecule type: protein
A;Residues: 35-54 <BE3>
A;Cross-references: UNIPARC:UPI0000172A3E
A;Experimental source: kidney
C;Superfamily: mammalian peptidyl-dipeptidase A

```
C;Keywords: alternative splicing; blood pressure control; membrane protein; peptidyldipe
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-1312/Product: peptidyl dipeptidase I #status predicted <MAT>

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  Best Local Similarity   42.6%;  Pred. No. 1.9e-87;
  Matches  255;  Conservative  112;  Mismatches  213;  Indels   18;  Gaps    7;

Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 61
              | | :|  |:::::  |: |  : : |:| |||||| |  : :      : |   : |
Db        649 TDEAKADRFVEEYDRTAQVLLNEYAEANWQYNTNITIEGSKILLEKSTEVSNHTLKYGTR 708

Qy         62 AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 121
              |: : :   || ::|  :: ||    :||   : :  | ||  | | ||   :|  :
Db        709 AKTFDVSNFQNSSIKRIIKKLQNLDRAVLPPKELEEYNQILLDMETTYSLSNICYTNG-- 766

Qy        122 ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 181
              |: ||| |  :|| |  | | ||||:||| :||: : | : :||   |::|: | | |
Db        767 TCMPLEPDLTNMMATSRKYEELLWAWKSWRDKVGRAILPFFPKYVEFSNKIAKLNGYTDA 826

Qy        182 GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 240
              || ||  || : ::          :|:|  ::|::||| :|||||  |   | | ||:
Db        827 GDSWRSLYESDNLE----------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 876

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              | :||||||:|| : |:|:| |  ||   |||| |:||: | |  :||||||: || |:
Db        877 DGPIPAHLLGNMWAQTWSNIYDLVAPFPSAPNIDATEAMIKQGWTPRRIFKEADNFFTSL 936

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG 359
              ||  :   ||  |||  | : :: ||||:|||   | ||||  || | |:| : ||||||
Db        937 GLLPVPPEFWNKSMLEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMG 996

Qy        360 HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 419
              |||| | |   |  | ||| |||||:|:||:|| :||||| |: ||| :     | :||
Db        997 HIQYFMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN 1055

Qy        420 FLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 479
              ||:| ||  :  :||:|::::||| || | | |: : ::|| :: :  |:  |||  :
Db       1056 FLMKMALDKIAFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGD 1115

Qy        480 CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM 539
              || | |||  :  ::||:   : |||| ||||:|| | |||||||||  | |||: | :
Db       1116 FDPGSKFHVPANVPYVRYFVSFIIQFQFHEALCRAAGHTGPLHKCDIYQSKEAGKLLADA 1175

Qy        540 LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 594
              ::|| |:||  |:: : |  ||:   ::|||:||  ||  :|:     :||   :|:|
Db       1176 MKLGYSKPWPEAMKLITGQPNMSASAMMNYFKPLTEWLVTENRRHGETLGWPEYNWAP 1233


RESULT 6
JC2038
peptidyl-dipeptidase A (EC 3.4.15.1) - rat
N;Alternate names: angiotensin converting enzyme; kininase II
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JC2038
R;Koike, G.; Krieger, J.E.; Jacob, H.J.; Mukoyama, M.; Pratt, R.E.; Dzau, V.J.
Biochem. Biophys. Res. Commun. 198, 380-386, 1994
A;Title: Angiotensin converting enzyme and genetic hypertension: Cloning of rat cDNAs ar
A;Reference number: JC2038; MUID:94121658; PMID:8292044
A;Accession: JC2038
A;Molecule type: mRNA
A;Residues: 1-1313 <KOI>
A;Cross-references: UNIPROT:P47820; UNIPARC:UPI000016828F; GB:U03734; NID:g437289; PIDN:
A;Note: the authors translated the codon ACC for residue 159 as Tyr
C;Comment: This enzyme is a zinc-containg dicarboxy peptidase that cleaves angiotensin I
C;Comment: This enzyme plays a critical role in blood pressure homeostasis and is the ta
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: alternative splicing; peptidyldipeptide hydrolase; transmembrane protein; zi
F;393-400,990-998/Region: catalytic #status predicted
F;1264-1284/Domain: transmembrane #status predicted <TMM>

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Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 61
              | | :|  |:::::  |: |: : : |:|:|||||| |  : :      : |    : |
Db        650 TDEAKANRFVEEYDRTAKVLWNEYAEANWHYNTNITIEGSKILLQKNKEVSNHTLKYGTW 709

Qy         62 AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 121
              |: : :   || |:|  :: :|    :||  :: :  | ||  | | ||   ||  :
Db        710 AKTFDVSNFQNSTIKRIIKKVQNVDRAVLPPNELEEYNQILLDMETTYSVANVCYTNG-- 767

Qy        122 ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 181
              || ||| |  ||| |  | | || |:||| :||: : | : :||   |::|: | | |
Db        768 TCLSLEPDLTNIMATSRKYEELLWVWKSWRDKVGRAILPFFPKYVDFSNKIAKLNGYSDA 827

Qy        182 GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 240
              || ||  || : ::          :|:|  ::|::||| :||||||  |   | | ||:
Db        828 GDSWRSSYESDDLE----------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 877

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              | :||||||:|| : |:|:| |  ||   |:|| |:||: | |  :||||||: || |:
Db        878 DGPIPAHLLGNMWAQTWSNIYDLVAPFPSAPSIDATEAMIKQGWTPRRIFKEADNFFTSL 937

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG 359
              ||  :   ||  |||  | : :: ||| :|||   | ||||  || | |:: : ||||||
Db        938 GLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTSVNMEELVIAHHEMG 997

Qy        360 HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 419
              |||| | |   |  | ||| |||||:|::::|| :||||| |: ||| :     | :||
Db        998 HIQYFMQYKDLPVTFREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSE-GSGYEHDIN 1056

Qy        420 FLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 479
              ||:| ||  :  :||:|::::||| || | | |: : ::|| :: :  |:  |||  :
Db       1057 FLMKMALDKIAFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGD 1116

Qy        480 CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM 539
              || | |||  :  :|||:   : |||| ||||:|| | |||:|||  | |||: | :
Db       1117 FDPGSKFHVPANVPYIRYFISFIIQFQFHEALCRAAGHTGPLYKCDIYQSKEAGKLLADA 1176

Qy        540 LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 594
              ::|| |: |  |:: : |  ||:   ::|||:||  ||  :|:     :||    |:|
Db       1177 MKLGYSKQWPEAMKIITGQPNMSASAIMNYFKPLTEWLVTENRRHGETLGWPEYTWTP 1234


RESULT 7
JC2489
peptidyl-dipeptidase A (EC 3.4.15.1) - chicken
N;Alternate names: angiotensin converting enzyme
C;Species: Gallus gallus (chicken)
C;Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JC2489
R;Esther, C.R.; Thomas Jr., K.E.; Bernstein, K.E.
Biochem. Biophys. Res. Commun. 205, 1916-1921, 1994
A;Title: Chicken lacks the testis specific isozyme of angiotensin converting enzyme found
A;Reference number: JC2489; MUID:95110342; PMID:7811282
A;Accession: JC2489
A;Molecule type: mRNA
A;Residues: 1-1193 <EST>
A;Cross-references: UNIPROT:Q10751; UNIPARC:UPI000012521E; GB:L40175; NID:g685168; PIDN:
C;Comment: This enzyme is a zinc dependant dipeptidyl carboxypeptidase that cleaves a va
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: metal binding; peptidyldipeptide hydrolase; zinc
F;316,331,914,929/Binding site: zinc, catalytic (Glu, His, Glu, His) #status predicted

  Query Match             40.5%;  Score 1307;  DB 2;  Length 1193;
  Best Local Similarity   42.3%;  Pred. No. 1.4e-85;
  Matches  254;  Conservative  106;  Mismatches  216;  Indels   24;  Gaps    8;

Qy          4 EEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTLAQ 63
              | ||| || ::|  || ::   : ||| ||||||: | : |       |    |    |:
Db        544 EAQAKEFLSEYNSTAEVVWNAYTEASWEYNTNITDHNKEVMLEKNLAMSKHTIEYGMRAR 603

Qy         64 MYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDN---P 120
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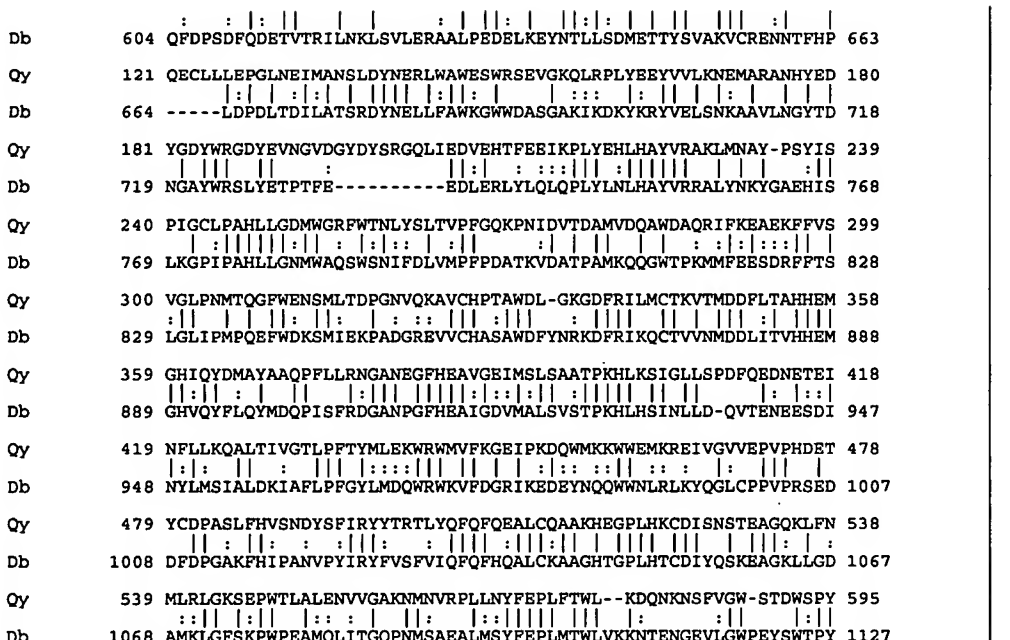
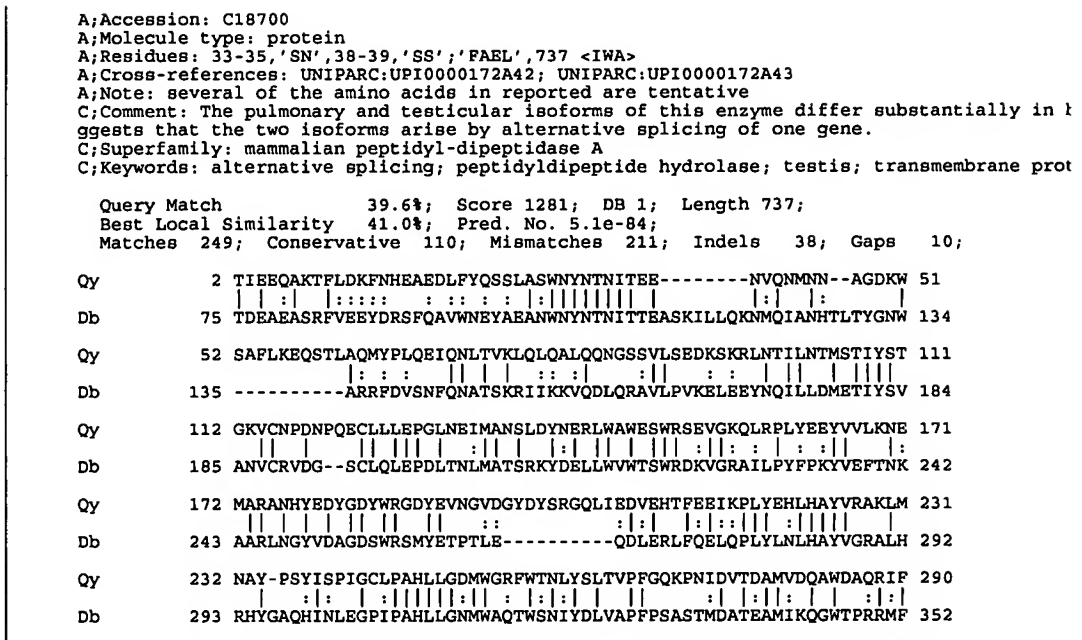


RESULT 8
A34402
peptidyl-dipeptidase A (EC 3.4.15.1) precursor, testicular - rabbit
N;Alternate names: angiotensin I-converting enzyme; dipeptidyl carboxypeptidase I; pepti
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A34402; A60724; A36232; C18700
R;Kumar, R.S.; Kusari, J.; Roy, S.N.; Soffer, R.L.; Sen, G.C.
J. Biol. Chem. 264, 16754-16758, 1989
A;Title: Structure of testicular angiotensin-converting enzyme. A segmental mosaic isozy
A;Reference number: A34402; MUID:89380303; PMID:2550457
A;Accession: A34402
A;Molecule type: mRNA
A;Residues: 1-737 <KUM>
A;Cross-references: UNIPROT:P22968; UNIPARC:UPI000004A558; GB:J05041; NID:g164744; PIDN:
R;Sen, G.C.; Thekkumkara, T.J.; Kumar, R.S.
J. Cardiovasc. Pharmacol. 16(Suppl.4), S14-S18, 1990
A;Title: Angiotensin-coverting enzyme: structural relationship of the testicular and the
A;Reference number: A60724; MUID:91155372; PMID:1705622
A;Accession: A60724
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 73-173 <SEN>
A;Cross-references: UNIPARC:UPI0000172A3F
A;Note: identical sequences were obtained for mRNAs from lung and testes
R;Chen, Y.N.P.; Riordan, J.F.
Biochemistry 29, 10493-10498, 1990
A;Title: Identification of essential tyrosine and lysine residues in angiotensin convert
A;Reference number: A36232; MUID:91104959; PMID:2176870
A;Accession: A36232
A;Molecule type: protein
A;Residues: 154-160;236-242 <CHE>
A;Cross-references: UNIPARC:UPI0000172A40; UNIPARC:UPI0000172A41
R;Iwata, K.; Lai, C.Y.; El-Dorry, H.A.; Soffer, R.L.
Biochem. Biophys. Res. Commun. 107, 1097-1103, 1982
A;Title: The NH2-and COOH-terminal sequences of the angiotensin-converting enzyme isozym
A;Reference number: A90107; MUID:83048249; PMID:6291514
A;Accession: C18700
A;Molecule type: protein
A;Residues: 33-35,'SN',38-39,'SS';'FAEL',737 <IWA>
A;Cross-references: UNIPARC:UPI0000172A42; UNIPARC:UPI0000172A43
A;Note: several of the amino acids in reported are tentative
C;Comment: The pulmonary and testicular isoforms of this enzyme differ substantially in t
ggests that the two isoforms arise by alternative splicing of one gene.
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: alternative splicing; peptidyldipeptide hydrolase; testis; transmembrane prot



RESULT 9
S35484
peptidyl-dipeptidase A (EC 3.4.15.1) precursor, pulmonary splice form - rabbit
N;Alternate names: angiotensin-converting enzyme; dipeptidyl carboxypeptidase I; kininase
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Dec-2004
C;Accession: S35484; A23455; A18700; A38655; A49726; S17509
R;Thekkumkara, T.J.; Livingston III, W.; Kumar, R.S.; Sen, G.C.
Nucleic Acids Res. 20, 683-687, 1992
A;Title: Use of alternative polyadenylation sites for tissue-specific transcription of tv
A;Reference number: S35484; MUID:92178960; PMID:1311831
A;Accession: S35484
A;Molecule type: mRNA
A;Residues: 1-1309 <THE>

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A;Cross-references: UNIPROT:P12822; UNIPROT:Q9TRW7; UNIPARC:UPI0000172A44; EMBL:X62551
R;Iwata, K.; Blacher, R.; Soffer, R.L.; Lai, C.Y.
Arch. Biochem. Biophys. 227, 188-201, 1983
A;Reference number: A23455; MUID:84051289; PMID:6314908
A;Accession: A23455
A;Molecule type: protein
A;Residues: 34-47,'N',49-55 <IWA>
A;Cross-references: UNIPARC:UPI0000172A45
A;Experimental source: lung
R;Iwata, K.; Lai, C.Y.; El-Dorry, H.A.; Soffer, R.L.
Biochem. Biophys. Res. Commun. 107, 1097-1103, 1982
A;Title: The NH2-and COOH-terminal sequences of the angiotensin-converting enzyme isozym
A;Reference number: A90107; MUID:83048249; PMID:6291514
A;Accession: A18700
A;Molecule type: protein
A;Residues: 34-44;754-755,'L',757 <IW2>
A;Cross-references: UNIPARC:UPI0000172A46; UNIPARC:UPI0000172A47
R;Kumar, R.S.; Thekkumkara, T.J.; Sen, G.C.
J. Biol. Chem. 266, 3854-3862, 1991
A;Title: The mRNAs encoding the two angiotensin-converting isozymes are transcribed from
A;Reference number: A38655; MUID:91139683; PMID:1847388
A;Accession: A38655
A;Molecule type: DNA
A;Residues: 1-88 <KUM>
A;Cross-references: UNIPARC:UPI0000172A48; GB:M58579
R;Ramchandran, R.; Sen, G.C.; Misono, K.; Sen, I.
J. Biol. Chem. 269, 2125-2130, 1994
A;Title: Regulated cleavage-secretion of the membrane-bound angiotensin-converting enzym
A;Reference number: A49726; MUID:94124568; PMID:8294466
A;Accession: A49726
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1236-1258 <RAM>
A;Cross-references: UNIPARC:UPI0000172A49
A;Experimental source: testis
R;Kirley, T.L.
Biochem. J. 278, 375-380, 1991
A;Title: The Mg(2+)-ATPase of rabbit skeletal-muscle transverse tubule is a highly glycc
A;Reference number: S17509; MUID:91378880; PMID:1654880
A;Accession: S17509
A;Status: preliminary
A;Molecule type: protein
A;Residues: 34-55 <KIR>
A;Cross-references: UNIPARC:UPI00000870D8
C;Comment: This enzyme converts angiotensin I to angiotensin II in presence of divalent
ver, the enzyme has been found also in renal tubules and intestinal mucosa.
C;Keywords: alternative splicing; blood pressure control; chloride; glycoprotein; intest
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-1309/Product: peptidyl-dipeptidase A, pulmonary #status experimental <MAT>
F;59,79,150,322,448,512,680,698,717,945,1194/Binding site: carbohydrate (Asn) (covalent)

  Query Match             39.6%;  Score 1281;  DB 1;  Length 1309;
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  Matches  249;  Conservative  110;  Mismatches  211;  Indels   38;  Gaps   10;

Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE--------NVQNMNN--AGDKW 51
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Db        647 TDEAEASRFVEEYDRSFQAVWNEYAEANWNYNTNITTEASKILLQKNMQIANHTLTYGNW 706

Qy         52 SAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYST 111
                        |: : :   || | |  :: :|    :||   : :  | ||  | ||||
Db        707 ----------ARRFDVSNFQNATSKRIIKKVQDLQRAVLPVKELEEYNQILLDMETIYSV 756

Qy        112 GKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNE 171
                 ||  |    || ||| |  :|| |  |:| || | ||| :||: : | : :||   |:
Db        757 ANVCRVDG--SCLQLEPDLTNLMATSRKYDELLWVWTSWRDKVGRAILPYFPKYVEFTNK 814

Qy        172 MARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLM 231
               || | | | || ||  ||   ::          :|:|  |:|::||| :|||||   |
Db        815 AARLNGYVDAGDSWRSMYETPTLE----------QDLERLFQELQPLYLNLHAYVGRALH 864

Qy        232 NAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIF 290
                 |   :|:  | :||||||:|| : |:|:| |  ||     :| |:||: | |  :|:|
Db        865 RHYGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVAPFPSASTMDATEAMIKQGWTPRRMF 924

Qy        291 KEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMD 349
              :||:|||:|:||  :   ||  |||  | : :: ||| :|||   | ||||  || | |:
Db        925 EEADKFFISLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNME 984

Qy        350 DFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPD 409
              | :  |||||||| | |    |  || ||| |||||:|::::|| :||||| || ||| :
Db        985 DLVVVHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSINLLSSE 1044

Qy        410 FQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGV 469
                    | :||||:| ||  :  :||:|::::||| || | | |: : ::|| :: :  |:
Db       1045 -GGGYEHDINFLMKMALDKIAFIPFSYLVDEWRWRVFDGSITKENYNQEWWSLRLKYQGL 1103

Qy        470 VEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNS 529
                | |  :   || : ||: :   :|||:   : |||| ||||:|| | |||| |||  |
Db       1104 CPPAPRSQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCKAAGHTGPLHTCDIYQS 1163

Qy        530 TEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQN--KNSFVG 587
               |||::| : ::|| |:||  |:: : |  ||:   ::|||:||  ||  :|      :|
Db       1164 KEAGKRLADAMKLGYSKPWPEAMKVITGQPNMSASAMMNYFKPLMDWLLTENGRHGEKLG 1223

Qy        588 W-STDWSP 594
                |    |:|
Db       1224 WPQYTWTP 1231


RESULT 10
S65472
peptidyl-dipeptidase A (EC 3.4.15.1) precursor - horn fly
N;Alternate names: angiotensin I-converting enzyme
C;Species: Haematobia irritans (horn fly)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S65472; S65431
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, P.
Eur. J. Biochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran
A;Reference number: S65431; MUID:96215437; PMID:8647080
A;Accession: S65472
A;Molecule type: DNA
A;Residues: 1-611 <WIJ>
A;Cross-references: UNIPROT:Q10715; UNIPARC:UPI0000125220; EMBL:L43965; NID:g908759; PIDN
A;Note: the source is designated as Haematobia irritans exigua
A;Accession: S65431
A;Molecule type: protein
A;Residues: 18,'P',20-42;75-77,'Q',79-81,'X',83-84;179-190 <WIW>
A;Cross-references: UNIPARC:UPI0000175B82; UNIPARC:UPI0000175B83; UNIPARC:UPI0000175B84
A;Note: the source is designated as Haematobia irritans exigua
C;Genetics:
A;Gene: ACE
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: glycoprotein; metal binding; peptidyldipeptide hydrolase; zinc
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-611/Product: peptidyl-dipeptidase A #status predicted <MAT>
F;53,196,531/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             32.6%;  Score 1054.5;  DB 2;  Length 611;
  Best Local Similarity   37.7%;  Pred. No. 7.4e-68;
  Matches  222;  Conservative  105;  Mismatches  239;  Indels   23;  Gaps    8;

Qy          1 STIEEQAKT-FLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQS 59
              :| ||   | :|   | |         :  || | :|||:|| :  |    : : |||| :
Db         18 ATKEEIVATEYLQNINKELAKHTNVETEVSWAYASNITDENERLRNEISAENAKFLKEVA 77

Qy         60 TLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDN 119
                 | :  :   :  |: | ::| : | | |  :    |  :|: | : ::  :||:  |
Db         78 KDIQKFNWRTYGSADVRRQFKSLSKTGYSALPAEDYAELLEVLSAMESNFAKVRVCDYKN 137

Qy        120 PQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHY 178
                :| | |:| : ||:  | |  | : |  :  :  :|  :|:|| |  : |: |::
Db        138 SAKCDLSLDPEIEEIITKSRDPEELKYYWTQFYDKAGTPTRSNFEKYVELNTKSAKLNNF 197

Qy        179 EDYGDYWRGDYEVNGVDGYDYSRGQLIED-VEHTFEEIKPLYEHLHAYVRAKLMNAY-PS 236
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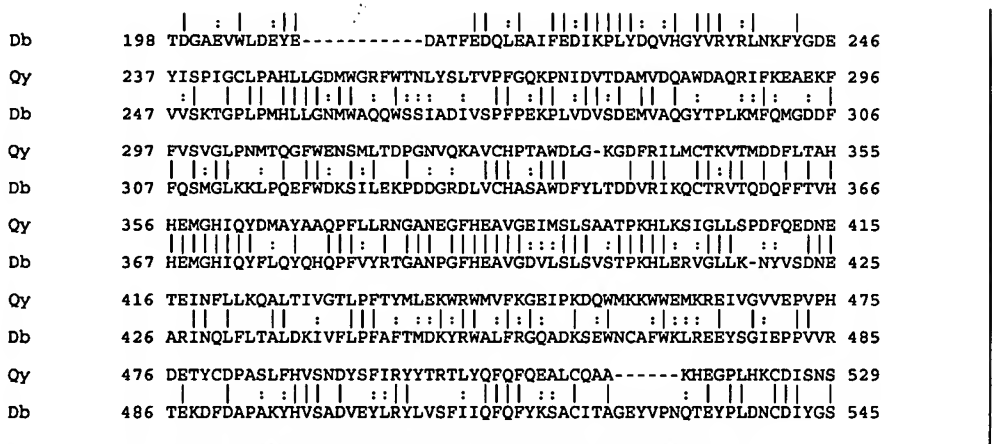
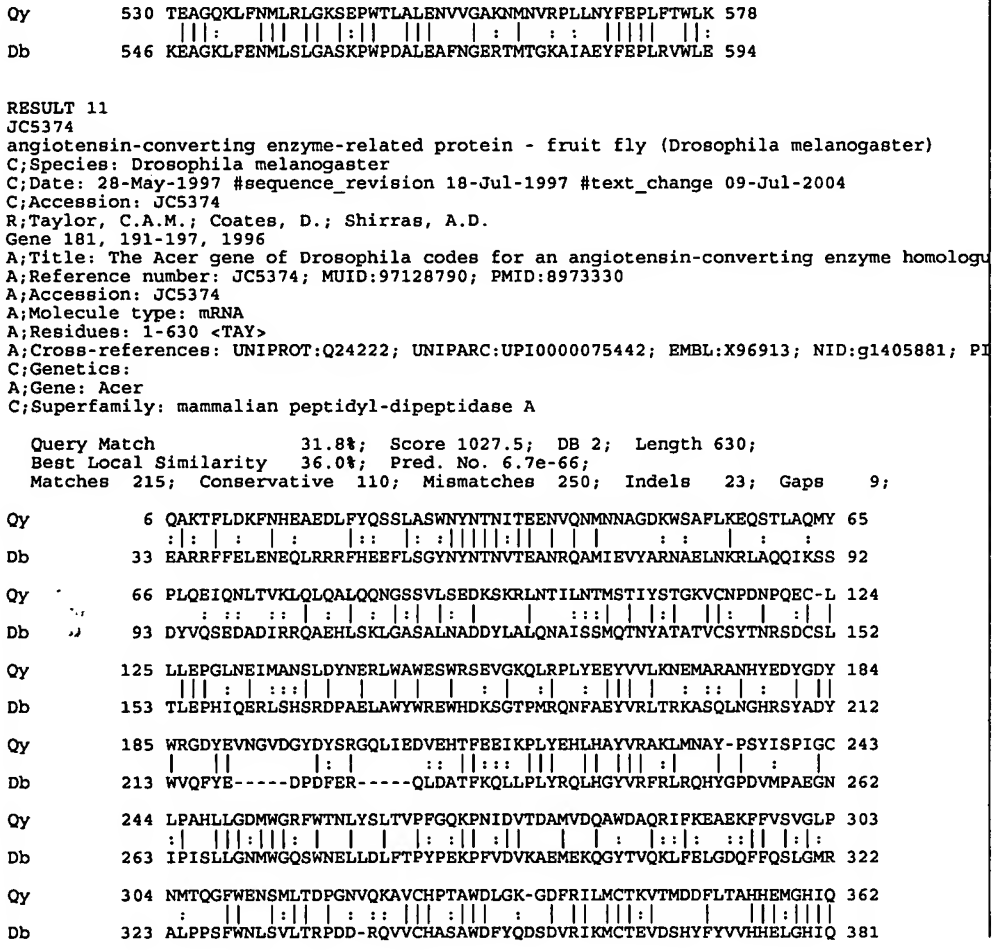
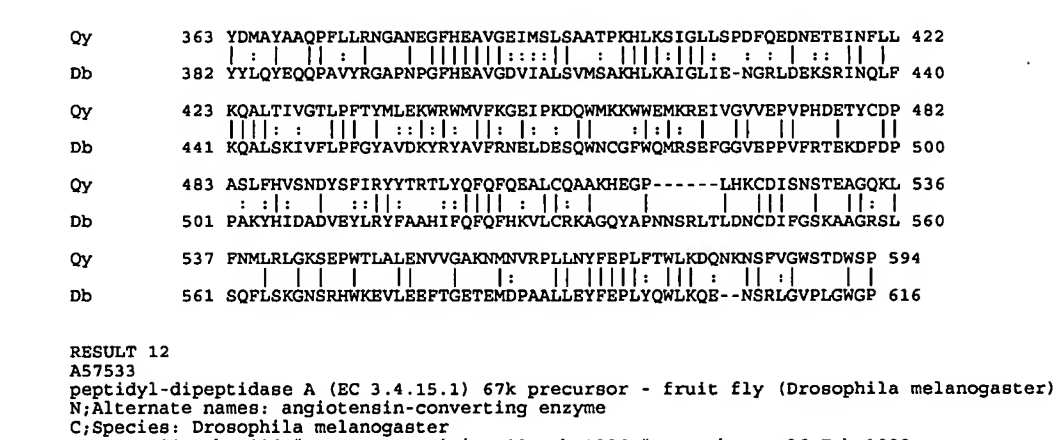


RESULT 11
JC5374
angiotensin-converting enzyme-related protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JC5374
R;Taylor, C.A.M.; Coates, D.; Shirras, A.D.
Gene 181, 191-197, 1996
A;Title: The Acer gene of Drosophila codes for an angiotensin-converting enzyme homologu
A;Reference number: JC5374; MUID:97128790; PMID:8973330
A;Accession: JC5374
A;Molecule type: mRNA
A;Residues: 1-630 <TAY>
A;Cross-references: UNIPROT:Q24222; UNIPARC:UPI0000075442; EMBL:X96913; NID:g1405881; PI
C;Genetics:
A;Gene: Acer
C;Superfamily: mammalian peptidyl-dipeptidase A

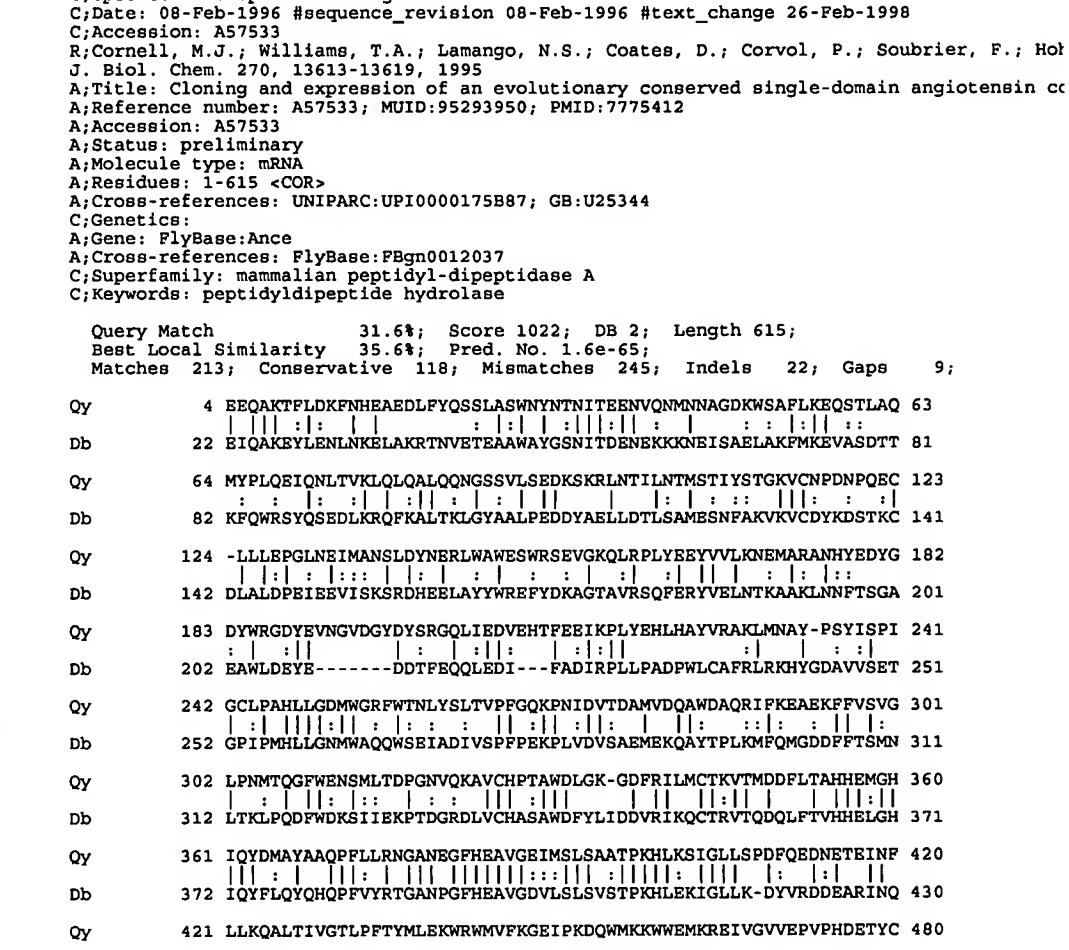
Query Match 31.8%; Score 1027.5; DB 2; Length 630;
Best Local Similarity 36.0%; Pred. No. 6.7e-66;
Matches 215; Conservative 110; Mismatches 250; Indels 23; Gaps 9;





RESULT 12
A57533
peptidyl-dipeptidase A (EC 3.4.15.1) 67k precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: angiotensin-converting enzyme
C;Species: Drosophila melanogaster
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 26-Feb-1998
C;Accession: A57533
R;Cornell, M.J.; Williams, T.A.; Lamango, N.S.; Coates, D.; Corvol, P.; Soubrier, F.; Hol
J. Biol. Chem. 270, 13613-13619, 1995
A;Title: Cloning and expression of an evolutionary conserved single-domain angiotensin cc
A;Reference number: A57533; MUID:95293950; PMID:7775412
A;Accession: A57533
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-615 <COR>
A;Cross-references: UNIPARC:UPI0000175B87; GB:U25344
C;Genetics:
A;Gene: FlyBase:Ance
A;Cross-references: FlyBase:FBgn0012037
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: peptidyldipeptide hydrolase

Query Match 31.6%; Score 1022; DB 2; Length 615;
Best Local Similarity 35.6%; Pred. No. 1.6e-65;
Matches 213; Conservative 118; Mismatches 245; Indels 22; Gaps 9;



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Db        431 LFLTALDKIVFLPFAFTMDKYRWSLFRGEVDKANWNCAFWKLRDEYSGIEPPVVRSEKDF 490

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALC-QAAKH-----EGPLHKCDISNSTEAGQ 534

Db        491 DAPAKYHISADVEYLRYLVSFIIQFQFYKSACIKAGQYDPDNVELPLDNCDIYGSARAGA 550

Qy        535 KLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQN--KNSFVGWST 590

Db        551 AFHNMLSMGASKPWPDALEAFNGERIMSGKAIAEYFEPLRVWLEAENIKNNVHIGWTT 608


RESULT 13
T15792
hypothetical protein C42D8.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15792
R;Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid C42D8.
A;Reference number: Z18405
A;Accession: T15792
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-907 <HAL>
A;Cross-references: UNIPROT:Q18581; UNIPARC:UPI000004A55C; EMBL:U56966; NID:g1293844; PI
A;Experimental source: strain Bristol N2; clone C42D8
C;Genetics:
A;Gene: CESP:C42D8.5
A;Map position: X
A;Introns: 140/3; 170/3; 194/3; 300/2; 467/3; 551/2; 600/2; 697/3; 774/2; 851/3

  Query Match             19.7%;  Score 635.5;  DB 2;  Length 907;
  Best Local Similarity   27.1%;  Pred. No. 1.8e-37;
  Matches  166;  Conservative  131;  Mismatches  277;  Indels   39;  Gaps   18;

Qy          4 EEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTLAQ 63

Db        178 EEKLRSWLAGYEAEAIKVLREVALSGWRYFNDASPSLKLALDEAENVLTMFVRSTSMQAK 237

Qy         64 MYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQEC 123

Db        238 QFDMASVTDEKVMRQLGYVSFEGMSALAPSRFADYSQAQAALNRDSKDSTICDKDVPPPC 297

Qy        124 LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYGD 183

Db        298 ALQKIDMDSIFRNEKDASRLQHLWVSYVTAIAKS-KPSYNNIITISNEGAKLNGFANGGA 356

Qy        184 YWRGDYEVNG-VDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY--PSYISP 240

Db        357 MWRSAFDMSSKVHKAEF---DLNKQIDKIYSTIQPFYQLLHAYMRRQLAGIYSNPVGLSK 413

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVD----QAWDAQRIFKEAEKF 296

Db        414 DGPIPAHLFGSLDGGDWSAHYEQTKPFEEES--ETPEAMLSAFNTQNYTTKKMFVTAYRY 471

Qy        297 FVSVGLPNMTQGFWENSMLTDPGNVQKAVCHP-TAWDL-GKGDFRILMCTKVTMDDFLTA 354

Db        472 FKSAGFPHLPKSYWTSSIFARVWS-KDMICHPAAALDMRAPNDFRVKACAQLGEPDFEQA 530

Qy        355 HHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDN 414

Db        531 HSLLVQTYYQYLYKDQSLLFREQASPVITDAIANAFAHLSTNPHYLYSQKLVPSEHLDIK 590

Qy        415 ETE-INFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPV 473

Db        591 DSVIINKLYKESLESFTKLPFTIAADNWRYELFDGTVPKNKLNDRWWEIRNKYEGVRSPQ 650

Qy        474 PHDETYCDPASLFH--VSNDYSFIRYYTRTL----YQFQFQEALCQAA---KHEGPLHKC 524

Db        651 PYNTSNLD--ALIHNSVSQVHS---PATRTLISYVLKFQILKALCQRELFWLSEG----C 701

Qy        525 DISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK-- 582

Db        702 ILSEDTT--EKLRETMKLGSSITWLKALEMISGKGELDAQPLLEYYEPLINWLRNTNEID 759

Qy        583 NSFVGWSTDWSPY 595

Db        760 QVVVGWDGEGTPF 772


RESULT 14
C83696
hypothetical protein BH0371 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C83696
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiram
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and g
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83696
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-532 <STO>
A;Cross-references: UNIPROT:Q9KFV0; UNIPARC:UPI00000C3863; GB:AP001508; GB:BA000004; NID:
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0371

  Query Match             4.9%;  Score 157;  DB 2;  Length 532;
  Best Local Similarity   21.1%;  Pred. No. 0.002;
  Matches  118;  Conservative   83;  Mismatches  213;  Indels  144;  Gaps   29;

Qy          4 EEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-NVQNMNNAGDKWSAFLKEQS--- 59

Db          3 EQDIERFLSEQNKRVEDLYQPVLLNHWMVATTGEQEWSDKHEQSLSEYWAHFSDRESFQK 62

Qy         60 ----------TLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIY 109

Db         63 VTRFRKIDSLPLMQRRQLDDLHDKMIKNQFE--EGTRQQILSLE--KKISHVFTTFQPQV 118

Qy        110 STGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLK 169

Db        119 NGSRVSNNE-----------LLDILRYDLDHERRKQAWFA-SKEVGKRTEKDLLQLIRKR 166

Qy        170 NEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHT---FEEIKPLYEHLHAYV 226

Db        167 NEVARNLGFETF--------------YHMSFATQELDLEQTFAMFETIKKSSDQAFRMI 211

Qy        227 -------RAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQK-PNIDVTDA 278

Db        212 KDEIDEERAKVLKIKKDDLRP------------------WDYVDPFFQEAPSIEHVD- 250

Qy        279 MVDQAWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQK-AVCHPTAWDLGKGD 337

Db        251 -FDSFYKDQDLEQVVSQTFQAMELP--IDDILKRSDLYPRKNKNPFGFC--TDMD-RRGD 304

Qy        338 FRILMCTKVTMDDFLTAHHEMGH-IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAAT 396

Db        305 IRVLLNLDQSMYWVTALLHEFGHAVYFKFIDSRLPFLLR------FH-------SHTLTT 351

Qy        397 PKHLKSIGLLS--PDFQE-----DNET------EINFLLKQALTIVGTLPFTYMLEKWRW 443

Db        352 EASALFFGRMTKMAEWYERFLGIDRETCERIGRNMEKMLQRQM-VVST----------RW 400

Qy        444 MV----FKG---EIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHVS------N 490

Db        401 MLTFSFFEKSLYEDPDQDINALWWKLVKEIQYMAP--PEDTGSPDWAAKMHFSLAPVYYQ 458

Qy        491 DY-------SFIRYYTRT 501

Db        459 DYLLGEMAASQLHHYIKT 476
```

RESULT 15
AF1310
probable thermostable carboxypeptidases homolog lmo1886 [imported] - Listeria monocytoge
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C;Accession: AF1310
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AF1310
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-502 <GLA>
A;Cross-references: UNIPROT:Q8Y616; UNIPARC:UPI00000CF1B7; GB:NC_003210; PIDN:CAC99964.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1886
C;Superfamily: Zn-dependent carboxypeptidase, Taq type

Query Match 4.8%; Score 154; DB 2; Length 502;
Best Local Similarity 20.1%; Pred. No. 0.003;
Matches 128; Conservative 101; Mismatches 215; Indels 192; Gaps 35;

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Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNT--------------NITEENVQNMNNA 47
              |:||:   :: |     | |    :|  |:  |                :  | : ||  :
Db          4 TLEEEFLAYIKKMEALEEAL----ALVYWDLRTGAPAKGMEGRSDVIGVLSEEIFNMQTS 59

Qy         48 GDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRL--------N 99
               :: :||:   :        |: :||: ::  : |::   |  : | :|::
Db         60 -EEMAAFIAGLN--------QDKENLS-EITRKTLEE---SQKTYDLNKKIPSKEYAEYT 106

Qy        100 TILNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLR 159
               ::    | ::| :  |     :    || | :|:
Db        107 KLVAQAETAWTTAREQN-----DFAAFEPFLTKIL------------------------ 136

Qy        160 PLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGY--DYSRGQLIEDVEHTFEEIKP 217
                        || |      : :||   || |  |     |  |  :  ::  ||:::
Db        137 -----------EMKR-----KFVEYW--GYEENKYDTLLDQYEPGVTVSVLDSVFEKVR- 177

Qy        218 LYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTD 277
              : : | :| |: |                                    | ||:  : :
Db        178 --DGIMA-IREKIENE---------------------------------GVKPDATILN 200

Qy        278 AMVDQAWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGD 337
              : :|       : ::| : : |  |  |       : | : : | || |  |  ||
Db        201 TKISEA--------KQKEFSIRI-LNKMGFDF-------EAGRLDETV-HPFATGLNTGD 243

Qy        338 FRILMCTKVTMDDFLTA----HHEMGHIQY----DMAYAAQPFLLRNGANEGFHEAVG-- 387
               ||   |:   :||  |     || ||  |    | |     |  | |||: | ||:
Db        244 VRI--TTRYNENDFKMAVFGTIHEGGHAIYEQNFDAALVGTP--LANGASMGIHESQSLF 299

Qy        388 -EIM---SLSAATPKHLKSIGLLSPDFQ----ED-----NETEINFLLKQALTIVGTLP- 433
               ||:   ||:     :     : | |     ||     | :| : :  :| |:  | |
Db        300 YEIIIGSSLAFWKSNYADFQAITKPAFDQVKLEDFYRAVNISESSLIRIEADTL--TYPL 357

Qy        434 ---FTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHVSN 490
                  | |||    :  ||:      | | :   | :|:    | ::|       :
Db        358 HIMIRYELEK---ALINGELEVKDLPKAWGDKYEEYLGI---RPDNDTNGVLQDIHWAGG 411

Qy        491 DYSFIRYYTRTL-YQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLF---NMLRLGKSE 546
              |: :   |   | | ||   :    : | |      |::   :  |::   :: : ||::
Db        412 DFGYFPSYALGLMYAAQFFNQM----QKEIPNIDAIIASDDYSELKIWLTEHVHKFGKTK 467

Qy        547 PWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK 582
                  | :  | : :|   ||:  |  : ::   ||
Db        468 KPLEILTDTTG-EGLNPTYLLDLLEKRYAYVYQFNK 502
```

Search completed: March 28, 2006, 11:17:18
Job time : 24.8626 secs

GenCore version 5.1.7


OM protein - protein search, using sw model

Run on: March 28, 2006, 11:03:07 ; Search time 124.785 Seconds
(without alignments)
3364.096 Million cell updates/sec

Title: US-10-659-000-4
Perfect score: 3231
Sequence: 1 STIEEQAKTFLDKFNHEAED.....WLKDQNKNSFVGWSTDWSPY 595

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 3231 | 100.0 | 805 | 1 | ACE2_HUMAN | Q9byf1 homo sapien |
| 2 | 3193 | 98.8 | 805 | 1 | ACE2_PONPY | Q5rfn1 pongo pygma |
| 3 | 2823 | 87.4 | 805 | 1 | ACE2_FELCA | Q56h28 felis silve |
| 4 | 2794 | 86.5 | 805 | 1 | ACE2_PAGLA | Q56nl1 paguma larv |
| 5 | 2757 | 85.3 | 805 | 1 | ACE2_RAT | Q5egz1 rattus norv |
| 6 | 2755 | 85.3 | 805 | 1 | ACE2_MOUSE | Q8r0i0 mus musculu |
| 7 | 2710.5 | 83.9 | 804 | 1 | ACE2_BOVIN | Q58dd0 bos taurus |
| 8 | 2018 | 62.5 | 785 | 2 | Q5U380_BRARE | Q5u380 brachydanio |
| 9 | 1613 | 49.9 | 652 | 2 | Q4SHR0_TETNG | Q4shr0 tetraodon n |
| 10 | 1345 | 41.6 | 1314 | 1 | ACE_MESAU | Q50je5 mesocricetu |
| 11 | 1335 | 41.3 | 732 | 1 | ACET_HUMAN | P22966 h angiotens |
| 12 | 1335 | 41.3 | 739 | 2 | Q8N710_HUMAN | Q8n710 homo sapien |
| 13 | 1335 | 41.3 | 1306 | 1 | ACE_HUMAN | P12821 homo sapien |
| 14 | 1334 | 41.3 | 732 | 1 | ACET_MOUSE | P22967 m angiotens |
| 15 | 1334 | 41.3 | 1015 | 2 | Q8K233_MOUSE | Q8k233 mus musculu |
| 16 | 1334 | 41.3 | 1187 | 2 | Q5XK22_MOUSE | Q5xk22 mus musculu |
| 17 | 1334 | 41.3 | 1312 | 1 | ACE_MOUSE | P09470 mus musculu |
| 18 | 1328 | 41.1 | 1144 | 2 | Q4S4M8_TETNG | Q4s4m8 tetraodon n |
| 19 | 1327 | 41.1 | 732 | 1 | ACET_PANTR | Q9gln6 p angiotens |
| 20 | 1327 | 41.1 | 1304 | 1 | ACE_PANTR | Q9gln7 pan troglod |
| 21 | 1310 | 40.5 | 775 | 1 | ACET_RAT | Q8cfn1 r angiotens |
| 22 | 1310 | 40.5 | 1313 | 1 | ACE_RAT | P47820 rattus norv |
| 23 | 1307 | 40.5 | 1193 | 1 | ACE_CHICK | Q10751 gallus gall |
| 24 | 1301 | 40.3 | 694 | 2 | Q15540_HUMAN | Q15540 homo sapien |
| 25 | 1295 | 40.1 | 724 | 2 | Q4W1E4_SHEEP | Q4w1e4 ovis aries |
| 26 | 1281 | 39.6 | 737 | 1 | ACET_RABIT | P22968 o angiotens |
| 27 | 1281 | 39.6 | 1310 | 1 | ACE_RABIT | P12822 oryctolagus |
| 28 | 1236 | 38.3 | 616 | 1 | ACE_THETS | Q6q4g4 theromyzon |
| 29 | 1176.5 | 36.4 | 625 | 2 | Q6RX62_LOCMI | Q6rx62 locusta mig |
| 30 | 1139.5 | 35.3 | 627 | 2 | Q5WPT4_LUTLO | Q5wpt4 lutzomyia l |
| 31 | 1092.5 | 33.8 | 619 | 2 | Q8EE93_SHEON | Q8ee93 shewanella |
| 32 | 1088 | 33.7 | 617 | 2 | Q7PM22_ANOGA | Q7pm22 anopheles g |
| 33 | 1078 | 33.4 | 648 | 2 | Q9NDS8_BOMMO | Q9nds8 bombyx mori |
| 34 | 1068 | 33.1 | 615 | 1 | ACE_DROME | Q10714 drosophila |
| 35 | 1054.5 | 32.6 | 611 | 1 | ACE_HAEIE | Q10715 haematobia |
| 36 | 1054 | 32.6 | 660 | 2 | Q17248_BOOMI | Q17248 boophilus m |
| 37 | 1025.5 | 31.7 | 630 | 1 | ACER_DROME | Q9vlj6 drosophila |
| 38 | 1005.5 | 31.1 | 614 | 2 | Q4NXG3_9DELT | Q4nxg3 anaeromyxob |
| 39 | 984.5 | 30.5 | 631 | 2 | Q7NGM5_GLOVI | Q7ngm5 gloeobacter |
| 40 | 965 | 29.9 | 672 | 2 | Q4URZ8_XANCP | Q4urz8 xanthomonas |
| 41 | 965 | 29.9 | 672 | 2 | Q8PBK3_XANCP | Q8pbk3 xanthomonas |
| 42 | 964 | 29.8 | 672 | 2 | Q8PN56_XANAC | Q8pn56 xanthomonas |
| 43 | 961 | 29.7 | 977 | 2 | Q7Q9W7_ANOGA | Q7q9w7 anopheles g |
| 44 | 949 | 29.4 | 686 | 2 | Q5GWX8_XANOR | Q5gwx8 xanthomonas |
| 45 | 943.5 | 29.2 | 567 | 2 | Q5VLH5_XANOR | Q5vlh5 xanthomonas |

ALIGNMENTS

RESULT 1
ACE2_HUMAN
ID ACE2_HUMAN STANDARD; PRT; 805 AA.
AC Q9BYF1; Q6UWP0; Q86WT0; Q9NRA7; Q9UFZ6;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Angiotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related
DE carboxypeptidase) (Angiotensin-converting enzyme homolog) (ACEH).
GN Name=ACE2; ORFNames=UNQ868/PRO1885;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), TISSUE SPECIFICITY, FUNCTION,
RP AND ENZYME REGULATION.
RC TISSUE=Heart;
RX MEDLINE=20429895; PubMed=10969042;
RA Donoghue M., Hsieh F., Baronas E., Godbout K., Gosselin M.,
RA Stagliano N., Donovan M., Woolf B., Robison K., Jeyaseelan R.,
RA Breitbart R.E., Acton S.;
RT "A novel angiotensin-converting enzyme-related carboxypeptidase (ACE2)
RT converts angiotensin I to angiotensin 1-9.";
RL Circ. Res. 87:E1-E9(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), TISSUE SPECIFICITY,
RP GLYCOSYLATION, FUNCTION, AND ENZYME REGULATION.
RC TISSUE=Lymphoma;
RX MEDLINE=20517872; PubMed=10924499; DOI=10.1074/jbc.M002615200;
RA Tipnis S.R., Hooper N.M., Hyde R., Karran E., Christie G.,
RA Turner A.J.;
RT "A human homolog of angiotensin-converting enzyme. Cloning and
RT functional expression as a captopril-insensitive carboxypeptidase.";
RL J. Biol. Chem. 275:33238-33243(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), TISSUE SPECIFICITY,
RP SUBCELLULAR LOCATION, AND ENZYME REGULATION.
RC TISSUE=Testis;
RX PubMed=15231706; DOI=10.1210/en.2004-0443;
RA Douglas G.C., O'Bryan M.K., Hedger M.P., Lee D.K.L., Yarski M.A.,
RA Smith A.I., Lew R.A.;
RT "The novel angiotensin-converting enzyme (ACE) homolog, ACE2, is
RT selectively expressed by adult Leydig cells of the testis.";
RL Endocrinology 145:4703-4711(2004).
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND VARIANT SER-638.
RC TISSUE=Lung, and Testis;
RX PubMed=15937940; DOI=10.1002/ajmg.a.30779;
RA Itoyama S., Keicho N., Hijikata M., Quy T., Phi N.C., Long H.T.,
RA Ha L.D., Ban V.V., Matsushita I., Yanai H., Kirikae F., Kirikae T.,
RA Kuratsuji T., Sasazuki T.;
RT "Identification of an alternative 5'-untranslated exon and new

RT polymorphisms of angiotensin-converting enzyme 2 gene: Lack of
RT association with SARS in the Vietnamese population.";
RL Am. J. Med. Genet. 136:52-57(2005).
RN [5]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RA Suzuki Y., Watanabe M., Sugano S.;
RT "Cloning, expression analysis and chromosomal localization of a novel
RT ACE like enzyme.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [7]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] (ISOFORM 1), AND VARIANT ARG-26.
RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
RA Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
RA Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Brain, and Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 2-805 (ISOFORM 1).
RC TISSUE=Testis;
RG The German cDNA consortium;
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN [10]
RP PROTEIN SEQUENCE OF 679-689, IDENTIFICATION BY MASS SPECTROMETRY, AND
RP INTERACTION WITH ITGB1.
RX PubMed=15276642; DOI=10.1016/j.bbadis.2004.05.005;
RA Lin Q., Keller R.S., Weaver B., Zisman L.S.;
RT "Interaction of ACE2 and integrin beta1 in failing human heart.";
RL Biochim. Biophys. Acta 1689:175-178(2004).
RN [11]
RP TISSUE SPECIFICITY.
RX MEDLINE=22347248; PubMed=12459472;
RA Harmer D., Gilbert M., Borman R., Clark K.L.;
RT "Quantitative mRNA expression profiling of ACE 2, a novel homologue of
RT angiotensin converting enzyme.";
RL FEBS Lett. 532:107-110(2002).
RN [12]
RP BIOPHYSICOCHEMICAL PROPERTIES, ENZYME REGULATION, AND COFACTOR.
RX PubMed=11815627; DOI=10.1074/jbc.M200581200;
RA Vickers C., Hales P., Kaushik V., Dick L., Gavin J., Tang J.,
RA Godbout K., Parsons T., Baronas E., Hsieh F., Acton S., Patane M.A.,
RA Nichols A., Tummino P.;
RT "Hydrolysis of biological peptides by human angiotensin-converting
RT enzyme-related carboxypeptidase.";
RL J. Biol. Chem. 277:14838-14843(2002).
RN [13]
RP FUNCTION, INTERACTION WITH HCOV-SARS S PROTEIN, GLYCOSYLATION, AND
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX PubMed=14647384; DOI=10.1038/nature02145;
RA Li W., Moore M.J., Vasilieva N., Sui J., Wong S.-K., Berne M.A.,
RA Somasundaran M., Sullivan J.L., Luzuriaga K., Greenough T.C., Choe H.,
RA Farzan M.;
RT "Angiotensin-converting enzyme 2 is a functional receptor for the SARS
RT coronavirus.";
RL Nature 426:450-454(2003).
RN [14]
RP INDUCTION.
RX PubMed=15151696; DOI=10.1186/1741-7015-2-19;
RA Goulter A.B., Goddard M.J., Allen J.C., Clark K.L.;
RT "ACE2 gene expression is up-regulated in the human failing heart.";
RL BMC Med. 2:19-19(2004).
RN [15]
RP TISSUE SPECIFICITY.
RX PubMed=15141377; DOI=10.1002/path.1570;
RA Hamming I., Timens W., Bulthuis M.L.C., Lely A.T., Navis G.J.,
RA van Goor H.;
RT "Tissue distribution of ACE2 protein, the functional receptor for SARS
RT coronavirus. A first step in understanding SARS pathogenesis.";
RL J. Pathol. 203:631-637(2004).
RN [16]
RP INTERACTION WITH HCOV-SARS S PROTEIN.
RX PubMed=15452268; DOI=10.1128/JVI.78.20.11429-11433.2004;
RA Li W., Greenough T.C., Moore M.J., Vasilieva N., Somasundaran M.,
RA Sullivan J.L., Farzan M., Choe H.;
RT "Efficient replication of severe acute respiratory syndrome
RT coronavirus in mouse cells is limited by murine angiotensin-converting
RT enzyme 2.";
RL J. Virol. 78:11429-11433(2004).
RN [17]
RP TISSUE SPECIFICITY, AND INDUCTION.
RX PubMed=15671045; DOI=10.1093/eurheartj/ehi114;
RA Burrell L.M., Risvanis J., Kubota E., Dean R.G., MacDonald P.S.,
RA Lu S., Tikellis C., Grant S.L., Lew R.A., Smith A.I., Cooper M.E.,
RA Johnston C.I.;
RT "Myocardial infarction increases ACE2 expression in rat and humans.";
RL Eur. Heart J. 26:369-375(2005).
RN [18]
RP INTERACTION WITH HCOV-SARS S PROTEIN, AND MUTAGENESIS.
RX PubMed=15791205; DOI=10.1038/sj.emboj.7600640;
RA Li W., Zhang C., Sui J., Kuhn J.H., Moore M.J., Luo S., Wong S.-K.,
RA Huang I.-C., Xu K., Vasilieva N., Murakami A., He Y., Marasco W.A.,
RA Guan Y., Choe H., Farzan M.;
RT "Receptor and viral determinants of SARS-coronavirus adaptation to
RT human ACE2.";
RL EMBO J. 24:1634-1643(2005).
RN [19]
RP PROTEOLYTIC CLEAVAGE.
RX PubMed=15983030; DOI=10.1074/jbc.M505111200;
RA Lambert D.W., Yarski M.A., Warner F.J., Thornhill P., Parkin E.T.,
RA Smith A.I., Hooper N.M., Turner A.J.;
RT "Tumor necrosis factor-alpha convertase (ADAM17) mediates regulated
RT ectodomain shedding of the SARS-CoV receptor, angiotensin-converting
RT enzyme-2 (ACE2).";
RL J. Biol. Chem. 280:0-0(2005).
RN [20]
RP INTERACTION WITH HCOV-NL63 S PROTEIN.

```
RX   PubMed=15897467; DOI=10.1073/pnas.0409465102;
RA   Hofmann H., Pyrc K., van der Hoek L., Geier M., Berkhout B.,

  Query Match           100.0%;  Score 3231;  DB 1;  Length 805;
  Best Local Similarity  100.0%;  Pred. No. 4.3e-220;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613


RESULT 2
ACE2_PONPY
ID   ACE2_PONPY     STANDARD;      PRT;   805 AA.
AC   Q5RFN1;
DT   13-SEP-2005 (Rel. 48, Created)
DT   13-SEP-2005 (Rel. 48, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Angiotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related
DE   carboxypeptidase).
GN   Name=ACE2;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Kidney;
RG   The German cDNA consortium;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Carboxypeptidase which converts angiotensin I to
CC       angiotensin 1-9, a peptide of unknown function, and angiotensin II
CC       to angiotensin 1-7, a vasodilator. Also able to hydrolyze apelin-
CC       13 and dynorphin-13 with high efficiency. May be an important
CC       regulator of heart function (By similarity).
CC   -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC   -!- COFACTOR: Binds 1 chloride ion per subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Processing by
CC       ADAM17 may lead to a secreted protein (By similarity).
CC   -!- SIMILARITY: Belongs to the peptidase M2 family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; CR857122; CAH89426.1; -; mRNA.
DR   SMR; Q5RFN1; 19-615.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR001548; Peptidase_M2.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Carboxypeptidase; Chloride; Glycoprotein; Hydrolase; Metal-binding;
KW   Metalloprotease; Protease; Signal; Transmembrane; Zinc.
FT   SIGNAL        1     17       Potential.
FT   CHAIN        18    805       Angiotensin-converting enzyme 2.
FT   TOPO_DOM     18    740       Extracellular (Potential).
FT   TRANSMEM    741    761       Potential.
FT   TOPO_DOM    762    805       Cytoplasmic (Potential).
FT   ACT_SITE    375    375       By similarity.
FT   ACT_SITE    505    505       By similarity.
FT   METAL       374    374       Zinc (catalytic) (By similarity).
FT   METAL       378    378       Zinc (catalytic) (By similarity).
FT   METAL       402    402       Zinc (catalytic) (By similarity).
FT   BINDING     169    169       Chloride (By similarity).
FT   BINDING     273    273       Substrate (By similarity).
FT   BINDING     345    345       Substrate (By similarity).
FT   BINDING     346    346       Substrate (By similarity).
FT   BINDING     371    371       Substrate (By similarity).
FT   BINDING     477    477       Chloride (By similarity).
FT   BINDING     481    481       Chloride (By similarity).
FT   BINDING     515    515       Substrate (By similarity).
FT   CARBOHYD     53     53       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     90     90       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    103    103       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    322    322       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    432    432       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    546    546       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    690    690       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    133    141       By similarity.
FT   DISULFID    344    361       By similarity.
FT   DISULFID    530    542       By similarity.
SQ   SEQUENCE   805 AA;  92605 MW;  9F68CC1ACBC763F1 CRC64;

  Query Match           98.8%;  Score 3193;  DB 1;  Length 805;
  Best Local Similarity  98.8%;  Pred. No. 2.1e-217;
  Matches  588;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
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Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPNNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||| ||||||||||||||||||||||||||||:|||||||||||||||
Db        199 YGDYWRGDYEVNGVDSYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLINAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
                 ||||||| ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQRFWENSMLTDPGNVQKVVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLLNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
                 |||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLDYFEPLFTWLKDQNKNSFVGWSTDWSPY 613


RESULT 3
ACE2_FELCA
ID   ACE2_FELCA     STANDARD;      PRT;   805 AA.
AC   Q56H28;
DT   13-SEP-2005 (Rel. 48, Created)
DT   13-SEP-2005 (Rel. 48, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Angiotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related
DE   carboxypeptidase).
GN   Name=ACE2;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Wang C., Guo A.Z., Chen H.C.;
RT   "Identification of cat ACE2 gene and its potential function as a SARS-
RT   CoV receptor.";
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Carboxypeptidase which converts angiotensin I to
CC       angiotensin 1-9, a peptide of unknown function, and angiotensin II
CC       to angiotensin 1-7, a vasodilator. Also able to hydrolyze apelin-
CC       13 and dynorphin-13 with high efficiency. May be an important
CC       regulator of heart function (By similarity).
CC   -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC   -!- COFACTOR: Binds 1 chloride ion per subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Processing by
CC       ADAM17 may lead to a secreted protein (By similarity).
CC   -!- SIMILARITY: Belongs to the peptidase M2 family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AY957464; AAX59005.1; -; mRNA.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR001548; Peptidase_M2.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Carboxypeptidase; Chloride; Glycoprotein; Hydrolase; Metal-binding;
KW   Metalloprotease; Protease; Signal; Transmembrane; Zinc.
FT   SIGNAL       1     17       Potential.
FT   CHAIN       18    805       Angiotensin-converting enzyme 2.
FT   TOPO_DOM    18    740       Extracellular (Potential).
FT   TRANSMEM    741   761       Potential.
FT   TOPO_DOM    762   805       Cytoplasmic (Potential).
FT   ACT_SITE    375   375       By similarity.
FT   ACT_SITE    505   505       By similarity.
FT   METAL       374   374       Zinc (catalytic) (By similarity).
FT   METAL       378   378       Zinc (catalytic) (By similarity).
FT   METAL       402   402       Zinc (catalytic) (By similarity).
FT   BINDING     169   169       Chloride (By similarity).
FT   BINDING     273   273       Substrate (By similarity).
FT   BINDING     345   345       Substrate (By similarity).
FT   BINDING     346   346       Substrate (By similarity).
FT   BINDING     371   371       Substrate (By similarity).
FT   BINDING     477   477       Chloride (By similarity).
FT   BINDING     481   481       Chloride (By similarity).
FT   BINDING     515   515       Substrate (By similarity).
FT   CARBOHYD     53    53       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     90    90       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    216   216       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    299   299       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    322   322       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    546   546       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    660   660       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    690   690       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    133   141       By similarity.
FT   DISULFID    344   361       By similarity.
FT   DISULFID    530   542       By similarity.
SQ   SEQUENCE   805 AA;  92708 MW;  9F41A2EF300BE19E CRC64;

  Query Match             87.4%;  Score 2823;  DB 1;  Length 805;
  Best Local Similarity   86.1%;  Pred. No. 3.6e-191;
  Matches  512;  Conservative   37;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              || || |||||:|||||||:| |||||||||||||||:|||| || || ||||| :|||
Db         19 STTEELAKTFLEKFNHEAEELSYQSSLASWNYNTNITDENVQKMNEAGAKWSAFYEEQSK 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||: ||| || | ||| ||||||||:|||||| |||:||||||| ||||||||| |||:||
Db         79 LAKTYPLAEIHNTTVKRQLQALQQSGSSVLSADKSQRLNTILNAMSTIYSTGKACNPNNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||::|| || |||||||||| ||:|||||||||||||| ||||||||:|||
Db        139 QECLLLEPGLDDIMENSKDYNERLWAWEGWRAEVGKQLRPLYEEYVALKNEMARANNYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              |||||||||    |||:||| |||:|||||| :|||||:||||||||||: ||| |||
Db        199 YGDYWRGDYEEEWTDGYNYSRSQLIKDVEHTFTQIKPLYQHLHAYVRAKLMDTYPSRISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              |||||||||||||||||| ||||||||||||||||:|:|||:|||||||||||||||
Db        259 TGCLPAHLLGDMWGRFWTNLYPLTVPFGQKPNIDVTDAMVNQSWDARRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||:||: :| |||||||||||||||| |||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTEPGDSRKVVCHPTAWDLGKGDFRIKMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              |||||||| |||||||||||||||||||||||||| |||:|||||| | ||:||||||
Db        379 IQYDMAYAVQPFLLRNGANEGFHEAVGEIMSLSAATPNHLKTIGLLSPGFSEDSETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              |||||||||||||||||||||||||||||:|||:|||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKEQWMQKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||:|||||||||||:||||||||: |||||||||||||:|||:||  ||
Db        499 DPASLFHVANDYSFIRYYTRTIYQFQFQEALCRIAKHEGPLHKCDISNSSEAGKKLLQML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||:|||||||:||| | ||| ||| ||||||||||:||:||||||:||| ||
Db        559 TLGKSKPWTLALEHVVGEKKMNVTPLLKYFEPLFTWLKEQNRNSFVGWNTDWRPY 613
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RESULT 4
ACE2_PAGLA
ID   ACE2_PAGLA     STANDARD;      PRT;   805 AA.
AC   Q56NL1;
DT   13-SEP-2005 (Rel. 48, Created)
DT   13-SEP-2005 (Rel. 48, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Angiotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related
DE   carboxypeptidase).
GN   Name=ACE2;
OS   Paguma larvata (Masked palm civet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Viverridae;
OC   Paradoxurinae; Paguma.
OX   NCBI_TaxID=9675;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND INTERACTION WITH HCOV-SARS S PROTEIN.
RX   PubMed=15791205; DOI=10.1038/sj.emboj.7600640;
RA   Li W., Zhang C., Sui J., Kuhn J.H., Moore M.J., Luo S., Wong S.-K.,
RA   Huang I.-C., Xu K., Vasilieva N., Murakami A., He Y., Marasco W.A.,
RA   Guan Y., Choe H., Farzan M.;
RT   "Receptor and viral determinants of SARS-coronavirus adaptation to
RT   human ACE2.";
RL   EMBO J. 24:1634-1643(2005).
CC   -!- FUNCTION: Carboxypeptidase which converts angiotensin I to
CC       angiotensin 1-9, a peptide of unknown function, and angiotensin II
CC       to angiotensin 1-7, a vasodilator. Also able to hydrolyze apelin-
CC       13 and dynorphin-13 with high efficiency. May be an important
CC       regulator of heart function (By similarity). Functional receptor
CC       for human coronavirus SARS.
CC   -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC   -!- COFACTOR: Binds 1 chloride ion per subunit (By similarity).
CC   -!- SUBUNIT: Interacts with HCOV-SARS S protein.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Processing by
CC       ADAM17 may lead to a secreted protein (By similarity).
CC   -!- SIMILARITY: Belongs to the peptidase M2 family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; AY881174; AAX63775.1; -; mRNA.
DR   InterPro; IPR010980; Cyt_c_b562.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR001548; Peptidase_M2.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Carboxypeptidase; Chloride; Glycoprotein; Hydrolase; Metal-binding;
KW   Metalloprotease; Protease; Signal; Transmembrane; Zinc.
FT   SIGNAL        1     17       Potential.
FT   CHAIN        18    805       Angiotensin-converting enzyme 2.
FT   TOPO_DOM     18    740       Extracellular (Potential).
FT   TRANSMEM    741    761       Potential.
FT   TOPO_DOM    762    805       Cytoplasmic (Potential).
FT   REGION       30     41       Interaction with SARS S protein.
FT   REGION       82     84       Interaction with SARS S protein (By
FT                                similarity).
FT   REGION       90     93       Interaction with SARS S protein.
FT   REGION      353    357       Interaction with SARS S protein (By
FT                                similarity).
FT   ACT_SITE    375    375       By similarity.
FT   ACT_SITE    505    505       By similarity.
FT   METAL       374    374       Zinc (catalytic) (By similarity).
FT   METAL       378    378       Zinc (catalytic) (By similarity).
FT   METAL       402    402       Zinc (catalytic) (By similarity).
FT   BINDING     169    169       Chloride (By similarity).
FT   BINDING     273    273       Substrate (By similarity).
FT   BINDING     345    345       Substrate (By similarity).
FT   BINDING     346    346       Substrate (By similarity).
FT   BINDING     371    371       Substrate (By similarity).
FT   BINDING     477    477       Chloride (By similarity).
FT   BINDING     481    481       Chloride (By similarity).
FT   BINDING     515    515       Substrate (By similarity).
FT   CARBOHYD     53     53       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    216    216       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    322    322       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    546    546       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    660    660       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    690    690       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    133    141       By similarity.
FT   DISULFID    344    361       By similarity.
FT   DISULFID    530    542       By similarity.
SQ   SEQUENCE   805 AA;  92611 MW;  CF6406851F73E378 CRC64;

  Query Match            86.5%;  Score 2794;  DB 1;  Length 805;
  Best Local Similarity  85.4%;  Pred. No. 4.1e-189;
  Matches  508;  Conservative   36;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              || || |||||: ||:||::| ||||:||||||||||:|| :||| || ||||: :|||
Db         19 STTEELAKTFLETFNYEAQELSYQSSVASWNYNTNITDENAKNMNEAGAKWSAYYEEQSK 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||| ||| |||:  :| |||||||:|||||| |||:|||||| |||||||||| |||:||
Db         79 LAQTYPLAEIQDAKIKRQLQALQQSGSSVLSADKSQRLNTILNAMSTIYSTGKACNPNNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              |||||||||: || || |||||||||| ||:|||||||||||||| |||||||||:|||
Db        139 QECLLLEPGLDNIMENSKDYNERLWAWEGWRAEVGKQLRPLYEEYVALKNEMARANNYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              |||||||||     ||:||| |||:||| |||:|||||:||||||||||: ||| ||
Db        199 YGDYWRGDYEEEWTGGYNYSRNQLIQDVEDTFEQIKPLYQHLHAYVRAKLMDTYPSRISR 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              |||||||||||||||||||| ||||||||||||||||:| |||:|||||||||||||
Db        259 TGCLPAHLLGDMWGRFWTNLYPLTVPFGQKPNIDVTDAMVNQNWDARRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              |||||||||||||||:||: :| |||||||||||||||| ||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTEPGDGRKVVCHPTAWDLGKGDFRIKMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              |||||||||||||||||||||||||||||||||||| |||:|||||| | |||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPNHLKTIGLLSPAFSEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              |||||||||||||||||||||||||||| |||:|||:||||||| ||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGAIPKEQWMQKWWEMKRNIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||:|||||||:|||||||||| |||||||||||||||||||||:||  ||
Db        499 DPASLFHVANDYSFIRYYTRTIYQFQFQEALCQIAKHEGPLHKCDISNSTEAGKKLLEML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
               ||:|||||||| |||||||| ||||||||||||:||:|||||| ||| ||
Db        559 SLGRSEPWTLALERVVGAKNMNVTPLLNYFEPLFTWLKEQNRNSFVGWDTDWRPY 613


RESULT 5
ACE2_RAT
ID   ACE2_RAT       STANDARD;      PRT;   805 AA.
AC   Q5EGZ1;
DT   13-SEP-2005 (Rel. 48, Created)
DT   13-SEP-2005 (Rel. 48, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Angiotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related
DE   carboxypeptidase).
GN   Name=Ace2;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
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OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], AND LACK OF INTERACTION WITH HCOV-SARS S
RP   PROTEIN.
RC   STRAIN=Sprague-Dawley;
RX   PubMed=15452268; DOI=10.1128/JVI.78.20.11429-11433.2004;
RA   Li W., Greenough T.C., Moore M.J., Vasilieva N., Somasundaran M.,
RA   Sullivan J.L., Farzan M., Choe H.;
RT   "Efficient replication of severe acute respiratory syndrome
RT   coronavirus in mouse cells is limited by murine angiotensin-converting
RT   enzyme 2.";
RL   J. Virol. 78:11429-11433(2004).
RN   [2]
RP   FUNCTION, AND INDUCTION.
RX   PubMed=12075344; DOI=10.1038/nature00786;
RA   Crackower M.A., Sarao R., Oudit G.Y., Yagil C., Kozieradzki I.,
RA   Scanga S.E., Oliveira-dos-Santos A.J., da Costa J., Zhang L., Pei Y.,
RA   Scholey J., Ferrario C.M., Manoukian A.S., Chappell M.C., Backx P.H.,
RA   Yagil Y., Penninger J.M.;
RT   "Angiotensin-converting enzyme 2 is an essential regulator of heart
RT   function.";
RL   Nature 417:822-828(2002).
RN   [3]
RP   ENZYME REGULATION, GLYCOSYLATION, TISSUE SPECIFICITY, AND SUBCELLULAR
RP   LOCATION.
RX   PubMed=15231706; DOI=10.1210/en.2004-0443;
RA   Douglas G.C., O'Bryan M.K., Hedger M.P., Lee D.K.L., Yarski M.A.,
RA   Smith A.I., Lew R.A.;
RT   "The novel angiotensin-converting enzyme (ACE) homolog, ACE2, is
RT   selectively expressed by adult Leydig cells of the testis.";
RL   Endocrinology 145:4703-4711(2004).
RN   [4]
RP   TISSUE SPECIFICITY, AND INDUCTION.
RX   PubMed=15671045; DOI=10.1093/eurheartj/ehi114;
RA   Burrell L.M., Risvanis J., Kubota E., Dean R.G., MacDonald P.S.,
RA   Lu S., Tikellis C., Grant S.L., Lew R.A., Smith A.I., Cooper M.E.,
RA   Johnston C.I.;
RT   "Myocardial infarction increases ACE2 expression in rat and humans.";
RL   Eur. Heart J. 26:369-375(2005).
RN   [5]
RP   TISSUE SPECIFICITY.
RX   PubMed=15949646; DOI=10.1016/j.peptides.2005.01.009;
RA   Gembardt F., Sterner-Kock A., Imboden H., Spalteholz M., Reibitz F.,
RA   Schultheiss H.-P., Siems W.-E., Walther T.;
RT   "Organ-specific distribution of ACE2 mRNA and correlating peptidase
RT   activity in rodents.";
RL   Peptides 26:1270-1277(2005).
CC   -!- FUNCTION: Carboxypeptidase which converts angiotensin I to
CC       angiotensin 1-9, a peptide of unknown function, and angiotensin II
CC       to angiotensin 1-7, a vasodilator. Also able to hydrolyze apelin-
CC       13 and dynorphin-13 with high efficiency. May be an important
CC       regulator of heart function.
CC   -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC   -!- COFACTOR: Binds 1 chloride ion per subunit (By similarity).
CC   -!- ENZYME REGULATION: Activated by chloride and fluoride, but not
CC       bromide. Inhibited by MLN-4760, cFP_Leu, and EDTA, but not by the
CC       ACE inhibitors linosipril, captopril, enalaprilat.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Processing by
CC       ADAM17 may lead to a secreted protein (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed in heart, kidney and forebrain. In
CC       testis, expression is restricted to Leydig cells. In heart,
CC       expressed in endothelial cells from small and large arteries,
CC       arterial smooth muscle cells, and myocytes (at protein level).
CC       Ubiquitously expressed, with highest levels in ileum, bladder and
CC       lung.
CC   -!- INDUCTION: Down-regulated in hypertensive animals. Up-regulated
CC       after myocardial infarction.
CC   -!- PTM: Glycosylated.
CC   -!- MISCELLANEOUS: In contrast to its human and palm-civet orthologs,
CC       does not interact with HCOV-SARS S protein.
CC   -!- SIMILARITY: Belongs to the peptidase M2 family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AY881244; AAW78017.1; -; mRNA.
DR   RGD; 728890; Ace2.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR001548; Peptidase_M2.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 1.
DR   PROSITE; PS00678; WD_REPEATS_1; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Carboxypeptidase; Chloride; Glycoprotein; Hydrolase; Metal-binding;
KW   Metalloprotease; Protease; Signal; Transmembrane; Zinc.
FT   SIGNAL        1    17       Potential.
FT   CHAIN        18   805       Angiotensin-converting enzyme 2.
FT   TOPO_DOM     18   740       Extracellular (Potential).
FT   TRANSMEM    741   761       Potential.
FT   TOPO_DOM    762   805       Cytoplasmic (Potential).
FT   ACT_SITE    375   375       By similarity.
FT   ACT_SITE    505   505       By similarity.
FT   METAL       374   374       Zinc (catalytic) (By similarity).
FT   METAL       378   378       Zinc (catalytic) (By similarity).
FT   METAL       402   402       Zinc (catalytic) (By similarity).
FT   BINDING     169   169       Chloride (By similarity).
FT   BINDING     273   273       Substrate (By similarity).
FT   BINDING     345   345       Substrate (By similarity).
FT   BINDING     346   346       Substrate (By similarity).
FT   BINDING     371   371       Substrate (By similarity).
FT   BINDING     477   477       Chloride (By similarity).
FT   BINDING     481   481       Chloride (By similarity).
FT   BINDING     515   515       Substrate (By similarity).
FT   CARBOHYD     53    53       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     82    82       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     90    90       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    299   299       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    432   432       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    546   546       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    601   601       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    660   660       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    690   690       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    133   141       By similarity.
FT   DISULFID    344   361       By similarity.
FT   DISULFID    530   542       By similarity.
SQ   SEQUENCE   805 AA;  92491 MW;  A4079F2407960D28 CRC64;

  Query Match           85.3%;  Score 2757;  DB 1;  Length 805;
  Best Local Similarity   84.2%;  Pred. No. 1.7e-186;
  Matches  501;  Conservative   42;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              | |||:|::||:||| ||||| |||||||||||||||||| | || |  ||||| :|||
Db         19 SLIEEKAESFLNKFNQEAEDLSYQSSLASWNYNTNITEENAQKMNEAAAKWSAFYEEQSK 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              :|| : |||||| |:| ||:||||:||| || ||:|:|||||||||||||||||||  ||
Db         79 IAQNFSLQEIQNATIKRQLKALQQSGSSALSPDKNKQLNTILNTMSTIYSTGKVCNSMNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||| |||||:|||| | ||| |||||| ||:||||||||||||||||||||||:|||
Db        139 QECFLLEPGLDEIMATSTDYNRRLWAWEGWRAEVGKQLRPLYEEYVVLKNEMARANNYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              |||||||||  ||:||:|:| |||||||:||:||||||| |||||| |||  |||||||
Db        199 YGDYWRGDYEAEGVEGYNYNRNQLIEDVENTFKEIKPLYEQLHAYVRTKLMEVYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              |||||||||||||||||| || || ||||||||||||:|:|||:|||||||||||||||
Db        259 TGCLPAHLLGDMWGRFWTNLYPLTTPFLQKPNIDVTDAMVNQSWDAERIFKEAEKFFVSV 318
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Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||| || ||| |||||:||: :| |||||||||| ||||| ||||||||:||||||||||
Db        319 GLPQMTPGFWTNSMLTEPGDDRKVVCHPTAWDLGHGDFRIKMCTKVTMDNFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              |||||||| ||||||||||||||||||||||||||||||||||||  :||||||||||||
Db        379 IQYDMAYAKQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLPSNFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              |||||||||||||||||||||||||||||: :||::|| |||||||||||||||:|||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFQDKIPREQWTKKWWEMKREIVGVVEPLPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              |||||||||||||||||||:|||||||||||||:|||||||||||||||||||||| |||
Db        499 DPASLFHVSNDYSFIRYYTRTIYQFQFQEALCQAAKHDGPLHKCDISNSTEAGQKLLNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              || | |||||||||||::||:|:||||||:||| |||:||:|| ||||||||||
Db        559 SLGNSGPWTLALENVVGSRNMDVKPLLNYFQPLFVWLKEQNRNSTVGWSTDWSPY 613


RESULT 6
ACE2_MOUSE
ID   ACE2_MOUSE     STANDARD;      PRT;   805 AA.
AC   Q8R0I0; Q99N70; Q99N71;
DT   13-SEP-2005 (Rel. 48, Created)
DT   13-SEP-2005 (Rel. 48, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Angiotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related
DE   carboxypeptidase).
GN   Name=Ace2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
RX   MEDLINE=22375506; PubMed=12487024; DOI=10.1080/1042517021000021608;
RA   Komatsu T., Suzuki Y., Imai J., Sugano S., Hida M., Tanigami A.,
RA   Muroi S., Yamada Y., Hanaoka K.;
RT   "Molecular cloning, mRNA expression, and chromosomal localization of
RT   mouse angiotensin-converting enzyme-related carboxypeptidase
RT   (mACE2).";
RL   DNA Seq. 13:217-220(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   STRAIN=FVB/N; TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   FUNCTION.
RX   PubMed=12075344; DOI=10.1038/nature00786;
RA   Crackower M.A., Sarao R., Oudit G.Y., Yagil C., Kozieradzki I.,
RA   Scanga S.E., Oliveira-dos-Santos A.J., da Costa J., Zhang L., Pei Y.,
RA   Scholey J., Ferrario C.M., Manoukian A.S., Chappell M.C., Backx P.H.,
RA   Yagil Y., Penninger J.M.;
RT   "Angiotensin-converting enzyme 2 is an essential regulator of heart
RT   function.";
RL   Nature 417:822-828(2002).
RN   [4]
RP   FUNCTION.
RX   MEDLINE=22848473; PubMed=12967627; DOI=10.1016/S0022-2828(03)00177-9;
RA   Donoghue M., Wakimoto H., Maguire C.T., Acton S., Hales P.,
RA   Stagliano N., Fairchild-Huntress V., Xu J., Lorenz J.N., Kadambi V.,
RA   Berul C.I., Breitbart R.E.;
RT   "Heart block, ventricular tachycardia, and sudden death in ACE2
RT   transgenic mice with downregulated connexins.";
RL   J. Mol. Cell. Cardiol. 35:1043-1053(2003).
RN   [5]
RP   INTERACTION WITH HCOV-SARS S PROTEIN.
RX   PubMed=15452268; DOI=10.1128/JVI.78.20.11429-11433.2004;
RA   Li W., Greenough T.C., Moore M.J., Vasilieva N., Somasundaran M.,
RA   Sullivan J.L., Farzan M., Choe H.;
RT   "Efficient replication of severe acute respiratory syndrome
RT   coronavirus in mouse cells is limited by murine angiotensin-converting
RT   enzyme 2.";
RL   J. Virol. 78:11429-11433(2004).
RN   [6]
RP   TISSUE SPECIFICITY, INDUCTION, AND FUNCTION.
RX   PubMed=16001071; DOI=10.1038/nature03712;
RA   Imai Y., Kuba K., Rao S., Huan Y., Guo F., Guan B., Yang P., Sarao R.,
RA   Wada T., Leong-Poi H., Crackower M.A., Fukamizu A., Hui C.-C.,
RA   Hein L., Uhlig S., Slutsky A.S., Jiang C., Penninger J.M.;
RT   "Angiotensin-converting enzyme 2 protects from severe acute lung
RT   failure.";
RL   Nature 436:112-116(2005).
RN   [7]
RP   TISSUE SPECIFICITY.
RX   PubMed=15949646; DOI=10.1016/j.peptides.2005.01.009;
RA   Gembardt F., Sterner-Kock A., Imboden H., Spalteholz M., Reibitz F.,
RA   Schultheiss H.-P., Siems W.-E., Walther T.;
RT   "Organ-specific distribution of ACE2 mRNA and correlating peptidase
RT   activity in rodents.";
RL   Peptides 26:1270-1277(2005).
CC   -!- FUNCTION: Carboxypeptidase which converts angiotensin I to
CC       angiotensin 1-9, a peptide of unknown function, and angiotensin II
CC       to angiotensin 1-7, a vasodilator. Also able to hydrolyze apelin-
CC       13 and dynorphin-13 with high efficiency. May be an important
CC       regulator of heart function. May have a protective role in acute
CC       lung injury.
CC   -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC   -!- COFACTOR: Binds 1 chloride ion per subunit (By similarity).
CC   -!- SUBUNIT: Weakly interacts with HCOV-SARS S protein.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Processing by
CC       ADAM17 may lead to a secreted protein (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q8R0I0-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q8R0I0-2; Sequence=VSP_014903;
CC   -!- TISSUE SPECIFICITY: Expressed in heart, kidney and forebrain (at
CC       protein level). Ubiquitously expressed, with highest levels in
CC       ileum, kidney and lung. In lung, expressed on vascular endothelial
CC       and airway epithelial cells.
CC   -!- INDUCTION: Down-regulated in lung after acute injury.
CC   -!- MISCELLANEOUS: Mice lacking ACE2 are viable and fertile, exhibit
CC       normal kidney and lung function, but show a severe reduction in
CC       cardiac contractility, and are highly sensitive to severe acute
CC       lung failure. Transgenic mice overexpressing ACE2 in the heart
CC       appear healthy but show conduction disturbances and ventricular
CC       arrhythmias which can lead to sudden death.
CC   -!- CAUTION: Ref.1 (BAB40431) sequence differs from that shown due to
CC       a frameshift in position 784.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -------------------------------------------------------------------------
DR   EMBL; AB053181; BAB40431.1; ALT_FRAME; mRNA.
DR   EMBL; AB053182; BAB40432.1; -; mRNA.
DR   EMBL; BC026801; AAH26801.1; -; mRNA.
DR   HSSP; Q10714; 1J37.
DR   SMR; Q8R0I0; 19-615.
DR   MEROPS; M02.006; -.
DR   Ensembl; ENSMUSG00000015405; Mus musculus.
DR   MGI; MGI:1917258; Ace2.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0004180; F:carboxypeptidase activity; TAS.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR001548; Peptidase_M2.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 1.
DR   PROSITE; PS00678; WD_REPEATS_1; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Alternative splicing; Carboxypeptidase; Chloride; Glycoprotein;
KW   Hydrolase; Metal-binding; Metalloprotease; Protease; Signal;
KW   Transmembrane; Zinc.
FT   SIGNAL        1     17       Potential.
FT   CHAIN        18    805       Angiotensin-converting enzyme 2.
FT   TOPO_DOM     18    740       Extracellular (Potential).
FT   TRANSMEM    741    761       Potential.
FT   TOPO_DOM    762    805       Cytoplasmic (Potential).
FT   ACT_SITE    375    375       By similarity.
FT   ACT_SITE    505    505       By similarity.
FT   METAL       374    374       Zinc (catalytic) (By similarity).
FT   METAL       378    378       Zinc (catalytic) (By similarity).
FT   METAL       402    402       Zinc (catalytic) (By similarity).
FT   BINDING     169    169       Chloride (By similarity).
FT   BINDING     273    273       Substrate (By similarity).
FT   BINDING     345    345       Substrate (By similarity).
FT   BINDING     346    346       Substrate (By similarity).
FT   BINDING     371    371       Substrate (By similarity).
FT   BINDING     477    477       Chloride (By similarity).
FT   BINDING     481    481       Chloride (By similarity).
FT   BINDING     515    515       Substrate (By similarity).
FT   CARBOHYD     53     53       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    536    536       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    546    546       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    660    660       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    690    690       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    133    141       By similarity.
FT   DISULFID    344    361       By similarity.
FT   DISULFID    530    542       By similarity.
FT   VARSPLIC    354    805       Missing (in isoform 2).
FT                                /FTId=VSP_014903.
FT   CONFLICT    167    167       G -> S (in Ref. 1; BAB40432).
FT   CONFLICT    352    352       G -> E (in Ref. 1; BAB40432).
FT   CONFLICT    779    779       N -> S (in Ref. 1; BAB40431).
SQ   SEQUENCE   805 AA;  92368 MW;  D8B883AAC966A8D9 CRC64;

  Query Match             85.3%;  Score 2755;  DB 1;  Length 805;
  Best Local Similarity   84.2%;  Pred. No. 2.4e-186;
  Matches  501;  Conservative   37;  Mismatches   57;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              |  || |||||: || ||||| |||||||||||||||||| | |: |  ||||| :|||
Db         19 SLTEENAKTFLNNFNQEAEDLSYQSSLASWNYNTNITEENAQKMSEAAAKWSAFYEEQSK 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
                 || : |||||   :| |||||||:||| || ||:|:|||||||||||||||||||| ||
Db         79 TAQSFSLQEIQTPIIKRQLQALQQSGSSALSADKNKQLNTILNTMSTIYSTGKVCNPKNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
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                ||||||||||:|||| | ||| |||||| ||:||||||||||||||||||||||:| |
Db        139 QECLLLEPGLDEIMATSTDYNSRLWAWEGWRAEVGKQLRPLYEEYVVLKNEMARANNYND 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              |||||||||| | |||:|:| ||||||| || |||||||||||||| |||: |||||||
Db        199 YGDYWRGDYEAEGADGYNYNRNQLIEDVERTFAEIKPLYEHLHAYVRRKLMDTYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              |||||||||||||||||||| ||||| ||||||||||::| |||:|||:|||||||||
Db        259 TGCLPAHLLGDMWGRFWTNLYPLTVPFAQKPNIDVTDAMMNQGWDAERIFQEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              |||:|||||| |||||:| : :| |||||||||| ||||| |||||||:||||||||||
Db        319 GLPHMTQGFWANSMLTEPADGRKVVCHPTAWDLGHGDFRIKMCTKVTMDNFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              |||||||| ||||||||||||||||||||||||||||||||||  |||||:||||||
Db        379 IQYDMAYARQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLPSDFQEDSETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              |||||||||||||||||||||||||:|||||:|||||||||||||||||:|||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFRGEIPKEQWMKKWWEMKREIVGVVEPLPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              |||||||||||||||||:|||||||||||||: | |||||||||||||||  ||
Db        499 DPASLFHVSNDYSFIRYYTRTIYQFQFQEALCQAAKYNGSLHKCDISNSTEAGQKLLKML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              || ||||| |||||||:||:|:|||||:||| |||:||:||||||:|:|||| 
Db        559 SLGNSEPWTKALENVVGARNMDVKPLLNYFQPLFDWLKEQNRNSFVGWNTEWSPY 613
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RESULT 7
ACE2_BOVIN
ID   ACE2_BOVIN     STANDARD;      PRT;   804 AA.
AC   Q58DD0;
DT   13-SEP-2005 (Rel. 48, Created)
DT   13-SEP-2005 (Rel. 48, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Angiotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related
DE   carboxypeptidase).
GN   Name=ACE2;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA   Harhay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keele J.W.,
RA   Snelling W.M., Weidmann R.T., Smith T.P.L.;
RT   "Sequencing and analysis of Bos taurus full-length insert cDNA
RT   clones.";
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Carboxypeptidase which converts angiotensin I to
CC       angiotensin 1-9, a peptide of unknown function, and angiotensin II
CC       to angiotensin 1-7, a vasodilator. Also able to hydrolyze apelin-
CC       13 and dynorphin-13 with high efficiency. May be an important
CC       regulator of heart function (By similarity).
CC   -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC   -!- COFACTOR: Binds 1 chloride ion per subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Processing by
CC       ADAM17 may lead to a secreted protein (By similarity).
CC   -!- SIMILARITY: Belongs to the peptidase M2 family.
CC   -------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -------------------------------------------------------------------------
DR   EMBL; BT021667; AAX46514.1; -; mRNA.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
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DR   InterPro; IPR001548; Peptidase_M2.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Carboxypeptidase; Chloride; Glycoprotein; Hydrolase; Metal-binding;
KW   Metalloprotease; Protease; Signal; Transmembrane; Zinc.
FT   SIGNAL        1     17       Potential.
FT   CHAIN        18    804       Angiotensin-converting enzyme 2.
FT   TOPO_DOM     18    739       Extracellular (Potential).
FT   TRANSMEM    740    760       Potential.
FT   TOPO_DOM    761    804       Cytoplasmic (Potential).
FT   ACT_SITE    374    374       By similarity.
FT   ACT_SITE    504    504       By similarity.
FT   METAL       373    373       Zinc (catalytic) (By similarity).
FT   METAL       377    377       Zinc (catalytic) (By similarity).
FT   METAL       401    401       Zinc (catalytic) (By similarity).
FT   BINDING     168    168       Chloride (By similarity).
FT   BINDING     272    272       Substrate (By similarity).
FT   BINDING     344    344       Substrate (By similarity).
FT   BINDING     345    345       Substrate (By similarity).
FT   BINDING     370    370       Substrate (By similarity).
FT   BINDING     476    476       Chloride (By similarity).
FT   BINDING     480    480       Chloride (By similarity).
FT   BINDING     514    514       Substrate (By similarity).
FT   CARBOHYD     53     53       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     90     90       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    298    298       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    431    431       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    545    545       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    659    659       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    689    689       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    343    360       By similarity.
FT   DISULFID    529    541       By similarity.
SQ   SEQUENCE   804 AA;  93067 MW;  E81570A96872A963 CRC64;

  Query Match             83.9%;  Score 2710.5;  DB 1;  Length 804;
  Best Local Similarity   82.7%;  Pred. No. 3.4e-183;
  Matches  492;  Conservative   48;  Mismatches   54;  Indels    1;  Gaps    1;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              || |||||||||:|||||||| |||||||||||||||:|||| || |  ||||| :|||
Db         19 STTEEQAKTFLEKFNHEAEDLSYQSSLASWNYNTNITDENVQKMNEARAKWSAFYEEQSR 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
                :|: | |:||||||:| ||:||| :|:| || :|||||||||| |||||||||| :| |
Db         79 MAKTYSLEEIQNLTLKRQLKALQHSGTSALSAEKSKRLNTILNKMSTIYSTGKVLDP-NT 137

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              |||| |||||::|| || ||| |||||| ||:|||||||||||||||:|||||||:|||
Db        138 QECLALEPGLDDIMENSRDYNRRLWAWEGWRAEVGKQLRPLYEEYVVLENEMARANNYED 197

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              |||||||||| |   ||||| ||::||| || ||||||| |||||||||: |||||||
Db        198 YGDYWRGDYEVTGAGDYDYSRDQLMKDVERTFAEIKPLYEQLHAYVRAKLMHTYPSYISP 257

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              |||||||||||||||||||||||||  ||:|||| | :|:|||:||||||||||||:
Db        258 TGCLPAHLLGDMWGRFWTNLYSLTVPFEHKPSIDVTEKMENQSWDAERIFKEAEKFFVSI 317

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              || ||||||:|||||:||: :| |||||||||||||| ||||||||||||||||||
Db        318 SLPYMTQGFWDNSMLTEPGDGRKVVCHPTAWDLGKGDFRIKMCTKVTMDDFLTAHHEMGH 377

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              |||||||||:|||||||||||||||||||||||||| :||::|||:||| |||||||||
Db        378 IQYDMAYAAQPYLLRNGANEGFHEAVGEIMSLSAATPHYLKALGLLAPDFHEDNETEINF 437

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              |||||||||||||||||||||||||||||| |||:|||||||||||||:|||||||
Db        438 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKQQWMEKWWEMKREIVGVVEPLPHDETYC 497

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||| |||| |||||||||||:|||| |||| |||| | ||||||||||||:|  ||
Db        498 DPACLFHVAEDYSFIRYYTRTIYQFQFHEALCKTAKHEGALFKCDISNSTEAGQRLLQML 557

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              |||||||||||||:|| | |:|:|||||||||||||:|:|||||||:|:||
Db        558 RLGKSEPWTLALENIVGIKTMDVKPLLNYFEPLFTWLKEQNRNSFVGWSTEWTPY 612


RESULT 8
Q5U380_BRARE
ID   Q5U380_BRARE PRELIMINARY;      PRT;   785 AA.
AC   Q5U380;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Zgc:92514.
GN   Name=zgc:92514;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RG   NIH MGC Project;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC085667; AAH85667.1; -; mRNA.
DR   ZFIN; ZDB-GENE-041114-6; zgc:92514.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR001548; Peptidase_M2.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   785 AA;  90862 MW;  71CDF94B8772BDB1 CRC64;

  Query Match             62.5%;  Score 2018;  DB 2;  Length 785;
  Best Local Similarity   61.4%;  Pred. No. 4e-134;
  Matches  366;  Conservative   82;  Mismatches  144;  Indels    4;  Gaps    3;

Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 61
              |:|::|: ||:||: || |: || :|||| |||:|::||      |   || :  : |
Db         19 TVEDRAREFLNKFDEEASDIMYQYTLASWAYNTDISQENADKEAEAYAIWSEYYNKMSEE 78

Qy         62 AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 121
                :  ||: :| :  :|:||| ||  ||  || ||:  |  |:: |||||:|  ||  |:|
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```
Db         79 SNAYPIDQISDPIIKMQLQKLQDKGSGALSPDKASELRNIMSEMSTIYNTATVCKIDDPT 138

Qy        122 ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 181

Db        139 DCQTLEPGLESIMAESRDYDERLHVWEGWRVATGMKMRPLYEKYVDLKNEAAKLNNYEDH 198

Qy        182 GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPI 241

Db        199 GDYWRGDYETIDDPKYSYSRDQVIEDARRIYKEILPLYKELHAYVRAKLQDVYPGHIGSD 258

Qy        242 GCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSVG 301

Db        259 ACLPAHLLGDMWGRFWTNLYPLMIPYPDRPDIDVSSAMVEQGWDEIRLFKEAEKFFMSVN 318

Qy        302 LPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLG-KGDFRILMCTKVTMDDFLTAHHEMGH 360

Db        319 MPAMFDNFWNNSMFIKP-EERDVVCHPTAWDMGNRKDFRIKMCTKVNMDDFLTVHHEMGH 377

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420

Db        378 NQYQMAYRNHPYLLRDGANEGFHEAVGEIMSLSAATPSHLQSLGLLPSDFKQDYETDINF 437

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480

Db        438 LLKQALTIVGTLPFTYMLEEWRWQVFKAKIPKDEWMQQWWQMKRELVGVAEAVPRDETYC 497

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540

Db        498 DPPALFHVSGDYSFIRYFTRTIYQFQFQEALCKAAGHTGPLYKCDITNSTKAGDKLRHML 557

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGWSTDWSP 594

Db        558 ELGRSMSWTRALEEVAGTTKMDSQPLLHYFSTLMEWLKEENQKNNRVPGWNVNVNP 613


RESULT 9
Q4SHR0_TETNG
ID   Q4SHR0_TETNG PRELIMINARY;      PRT;   652 AA.
AC   Q4SHR0;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 5 SCAF14581, whole genome shotgun sequence.
GN   ORFNames=GSTENG00018041001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01014581; CAF99822.1; -; Genomic_DNA.
SQ   SEQUENCE   652 AA;  75369 MW;  75784B3D18283309 CRC64;

  Query Match             49.9%;  Score 1613;  DB 2;  Length 652;
  Best Local Similarity   64.2%;  Pred. No. 1.6e-105;
  Matches  299;  Conservative   58;  Mismatches  105;  Indels    4;  Gaps    3;

Qy        134 MANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNG 193

Db          1 MANSRNYSERLHVWEGWRRTVGQKMRPLYEDYVDLKNEASKLNGFEDYGAYWRYNYETIE 60

Qy        194 VD-GYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDM 252

Db         61 EDPQFLYTRDELMKDVRSAYKEILPLYKELHAYVRARLMEVYPGHIEPDGPLPAHLLGDM 120

Qy        253 WGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPNMTQGFWEN 312

Db        121 WGRFWTNLYSLTTPYPDKTDIDVTETMVAKGWNETGIFQAAEDFFVSVGLYKMFPNFWEN 180

Qy        313 SMLTDPGNVQKAVCHPTAWDLG-KGDFRILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQP 371

Db        181 SMLTKPSDGRQVVCHPTAWDMGNREDFRIKMCSKVTMDDFLTAHHEMGHNQYQMAYRNLS 240

Qy        372 FLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLKQALTIVGT 431

Db        241 YPLRDGANEGFHEAVGEIMSLSAATPKHLQGLKLLPDNFTYDSETEINFLLKQALTIVAT 300

Qy        432 LPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHVSND 491

Db        301 LPFTYMLEEWRWQVFAGNITKDQWMKQWWEMKRELVGVMEAVPRDESYCDPPALFHVSGD 360

Qy        492 YSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLGKSEPWTLA 551

Db        361 YSFIRYFTRTIYQFQFQKALCDAAGHTGDLASCDITGSKAAGTKLRNMLELGRSQSWTRA 420

Qy        552 LENVVGAKNMNVRPLLNYFEPLFTWL--KDQNKNSFVGWSTDWSPY 595

Db        421 LKTISGDVRMNAAPLLDYFKKLHDWLIVENKNNNRTVGWKTETEPY 466


RESULT 10
ACE_MESAU
ID   ACE_MESAU      STANDARD;      PRT;  1314 AA.
AC   Q50JE5;
DT   13-SEP-2005 (Rel. 48, Created)
DT   13-SEP-2005 (Rel. 48, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
DE   (Dipeptidyl carboxypeptidase I) (Kininase II) [Contains: Angiotensin-
DE   converting enzyme, somatic isoform, soluble form].
GN   Name=Ace; Synonyms=Dcp1;
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Cricetinae; Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Uchide T.;
RT   "cDNA cloning of hamster angiotensin converting enzyme and mRNA
RT   expression in organs.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Converts angiotensin I to angiotensin II by release of
CC       the terminal His-Leu, this results in an increase of the
CC       vasoconstrictor activity of angiotensin. Also able to inactivate
CC       bradykinin, a potent vasodilator (By similarity).
CC   -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
CC       oligopeptide-|-Xaa-Yaa, when Xaa is not Pro, and Yaa is neither
CC       Asp nor Glu. Thus, conversion of angiotensin I to angiotensin II,
CC       with increase in vasoconstrictor activity, but no action on
CC       angiotensin II.
CC   -!- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
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CC   -!- COFACTOR: Binds 2 chloride ions per subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. A soluble form
CC       released by proteolysis also exists (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Somatic;
CC         IsoId=Q50JE5-1; Sequence=Displayed;
CC       Name=Testis-specific;
CC         IsoId=Q50JE5-2; Sequence=Not described;
CC   -!- PTM: Phosphorylated by CK2 on Ser-1307; which allows membrane
CC       retention (By similarity).
CC   -!- SIMILARITY: Belongs to the peptidase M2 family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AB212958; BAD98304.1; -; mRNA.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR001548; Peptidase_M2.
DR   Pfam; PF01401; Peptidase_M2; 2.
DR   PROSITE; PS00142; ZINC_PROTEASE; 2.
KW   Alternative splicing; Carboxypeptidase; Glycoprotein; Hydrolase;
KW   Metal-binding; Metalloprotease; Phosphorylation; Protease; Repeat;
KW   Signal; Transmembrane; Zinc.
FT   SIGNAL        1     35       By similarity.
FT   CHAIN        36   1314       Angiotensin-converting enzyme, somatic
FT                                isoform.
FT   CHAIN        36   1238       Angiotensin-converting enzyme, somatic
FT                                isoform, soluble form.
FT   PROPEP     1239   1314       Removed in secreted form (By similarity).
FT   TOPO_DOM     36   1265       Extracellular (Potential).
FT   TOPO_DOM   1283   1314       Cytoplasmic (Potential).
FT   REGION       36    636       Peptidase M2 1.
FT   REGION      637   1238       Peptidase M2 2.
FT   ACT_SITE    397    397       1 (By similarity).
FT   ACT_SITE    995    995       2 (By similarity).
FT   METAL       396    396       Zinc 1 (catalytic) (By similarity).
FT   METAL       400    400       Zinc 1 (catalytic) (By similarity).
FT   METAL       994    994       Zinc 2 (catalytic) (By similarity).
FT   METAL       998    998       Zinc 2 (catalytic) (By similarity).
FT   METAL      1022   1022       Zinc 2 (catalytic) (By similarity).
FT   BINDING     797    797       Chloride 1 (By similarity).
FT   BINDING     835    835       Chloride 2 (By similarity).
FT   BINDING    1096   1096       Chloride 1 (By similarity).
FT   BINDING    1100   1100       Chloride 1 (By similarity).
FT   BINDING    1133   1133       Chloride 2 (By similarity).
FT   MOD_RES    1307   1307       Phosphoserine (By similarity).
FT   CARBOHYD     44     44       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    117    117       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    324    324       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   1314 AA;  151595 MW;  74E29238E87F157E CRC64;

  Query Match             41.6%;  Score 1345;  DB 1;  Length 1314;
  Best Local Similarity   42.6%;  Pred. No. 4.1e-86;
  Matches  255;  Conservative  115;  Mismatches  210;  Indels   18;  Gaps    7;

Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 61
              | | :|: |:::::  |  |: : : |:| ||||||  |  : :     | :    :  ||
Db        650 TDETEAAERFVEEYDRTARVLWNEYAEANWQYNTNITLEASKILLQKNKKVANHTLKYGTL 709

Qy         62 AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 121
              |: : :   || |:|  :: :|    :||   : :  | ||  | | ||   ||  :
Db        710 AKKFDVSNFQNYTIKRIIKKVQNMDRAVLPPKELEEYNQILMDMETTYSIANVCYLNG-- 767

Qy        122 ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 181
               || ||| |  :|| |  | | || |:||| :||: : ||: :|| | |::|  | | |
Db        768 TCLHLEPDLTNVMATSRKYEELLWVWKSWRDKVGRAILPLFPKYVELSNKIAHLNGYADG 827

Qy        182 GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 240
              || ||  ||   ::          :|:|  ::|::||| :||||||  |   | | :|:

Db        828 GDSWRSSYESKSLE----------QDLEQLYQELQPLYLNLHAYVRRSLHRHYGSQHINL 877

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              | :|||||:|| : |:|:| |  ||    ||:| |:||: | |  :||||||: || |:
Db        878 DGPIPAHLLGNMWAQTWSNIYDLVAPFPSAPNLDATEAMIKQGWTPRRIFKEADDFFTSL 937

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG 359
              ||  ::: ||  ||| ||: :: ||| :|||   | ||||  || | |:| : ||||||
Db        938 GLLPVSEEFWNKSMLEKPGDGREVVCHASAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMG 997

Qy        360 HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 419
              |||| | |   |  | ||| |||||:|::::|| :||||| |: ||| :     | :||
Db        998 HIQYFMQYKDLPVTFREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSE-GGGYEHDIN 1056

Qy        420 FLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 479
              ||:| ||  :  :||:|::::||| || | | |: : ::|| :: :  |:  |||  :
Db       1057 FLMKMALDKIAFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQDD 1116

Qy        480 CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM 539
              || | |||  :  :|||:   : |||| ||||:|| | ||||||||  | |||: | :
Db       1117 FDPGSKFHVPANVPYIRYFVSFIIQFQFHEALCRAAGHTGPLHKCDIYQSKEAGKLLADT 1176

Qy        540 LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 594
              :::| |:||  |:: : |  ||:   ::|||:||  ||  :|:     :||   :|:|
Db       1177 MKMGYSKPWPEAMKLITGQPNMSASAMMNYFKPLTEWLVTENRRHGETLGWPEYNWTP 1234


RESULT 11
ACET_HUMAN
ID   ACET_HUMAN     STANDARD;      PRT;   732 AA.
AC   P22966;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Angiotensin-converting enzyme, testis-specific isoform precursor
DE   (EC 3.4.15.1) (EC 3.2.1.-) (ACE-T) (Dipeptidyl carboxypeptidase I)
DE   (Kininase II) [Contains: Angiotensin-converting enzyme, testis-
DE   specific isoform, soluble form].
GN   Name=ACE; Synonyms=DCP, DCP1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=90046671; PubMed=2554286;
RA   Ehlers M.R.W., Fox E.A., Strydom D.J., Riordan J.F.;
RT   "Molecular cloning of human testicular angiotensin-converting enzyme:
RT   the testis isozyme is identical to the C-terminal half of endothelial
RT   angiotensin-converting enzyme.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:7741-7745(1989).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=89338720; PubMed=2547653; DOI=10.1016/0014-5793(89)80897-X;
RA   Lattion A.L., Soubrier F., Allegrini J., Hubert C., Corvol P.,
RA   Alhenc-Gelas F.;
RT   "The testicular transcript of the angiotensin I-converting enzyme
RT   encodes for the ancestral, non-duplicated form of the enzyme.";
RL   FEBS Lett. 252:99-104(1989).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS PRO-32; GLY-49 AND
RP   SER-712.
RX   MEDLINE=99251580; PubMed=10319862; DOI=10.1038/8760;
RA   Rieder M.J., Taylor S.L., Clark A.G., Nickerson D.A.;
RT   "Sequence variation in the human angiotensin converting enzyme.";
RL   Nat. Genet. 22:59-62(1999).
RN   [4]
RP   ZINC-BINDING.
RX   MEDLINE=91308093; PubMed=1649623;
RA   Ehlers M.R.W., Riordan J.F.;
RT   "Angiotensin-converting enzyme: zinc- and inhibitor-binding
RT   stoichiometries of the somatic and testis isozymes.";
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RL   Biochemistry 30:7118-7126(1991).
RN   [5]
RP   DISULFIDE BONDS.
RX   MEDLINE=96302256; PubMed=8755737; DOI=10.1021/bi960243x;
RA   Sturrock E.D., Yu X.C., Wu Z., Biemann K., Riordan J.F.;
RT   "Assignment of free and disulfide-bonded cysteine residues in testis
RT   angiotensin-converting enzyme: functional implications.";
RL   Biochemistry 35:9560-9566(1996).
RN   [6]
RP   CARBOHYDRATE-LINKAGE SITES ASN-121; ASN-140; ASN-186; ASN-368 AND
RP   ASN-617, AND MASS SPECTROMETRY.
RX   PubMed=9013598;
RA   Yu X.C., Sturrock E.D., Wu Z., Biemann K., Ehlers M.R.W.,
RA   Riordan J.F.;
RT   "Identification of N-linked glycosylation sites in human testis
RT   angiotensin-converting enzyme and expression of an active
RT   deglycosylated form.";
RL   J. Biol. Chem. 272:3511-3519(1997).
RN   [7]
RP   TISSUE SPECIFICITY.
RX   PubMed=12459472;
RA   Harmer D., Gilbert M., Borman R., Clark K.L.;
RT   "Quantitative mRNA expression profiling of ACE 2, a novel homologue of
RT   angiotensin converting enzyme.";
RL   FEBS Lett. 532:107-110(2002).
RN   [8]
RP   BIOPHYSICOCHEMICAL PROPERTIES, AND CLEAVAGE SITE.
RX   PubMed=12542396; DOI=10.1042/BJ20021842;
RA   Gordon K., Redelinghuys P., Schwager S.L.U., Ehlers M.R.W.,
RA   Papageorgiou A.C., Natesh R., Acharya K.R., Sturrock E.D.;
RT   "Deglycosylation, processing and crystallization of human testis
RT   angiotensin-converting enzyme.";
RL   Biochem. J. 371:437-442(2003).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 68-656, AND X-RAY
RP   CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 68-656 IN COMPLEX WITH LISINOPRIL.
RX   PubMed=12540854; DOI=10.1038/nature01370;
RA   Natesh R., Schwager S.L.U., Sturrock E.D., Acharya K.R.;
RT   "Crystal structure of the human angiotensin-converting enzyme-
RT   lisinopril complex.";
RL   Nature 421:551-554(2003).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 68-656 IN COMPLEX WITH
RP   ENALAPRILAT, AND X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 68-656 IN
RP   COMPLEX WITH CAPTOPRIL.
RX   PubMed=15236580; DOI=10.1021/bi049480n;
RA   Natesh R., Schwager S.L.U., Evans H.R., Sturrock E.D., Acharya K.R.;
RT   "Structural details on the binding of antihypertensive drugs captopril
RT   and enalaprilat to human testicular angiotensin I-converting enzyme.";
RL   Biochemistry 43:8718-8724(2004).
CC   -!- FUNCTION: Converts angiotensin I to angiotensin II by release of
CC       the terminal His-Leu, this results in an increase of the
CC       vasoconstrictor activity of angiotensin. Also able to inactivate
CC       bradykinin, a potent vasodilator. Has also a glycosidase activity
CC       which releases GPI-anchored proteins from the membrane by cleaving
CC       the mannose linkage in the GPI moiety.
CC   -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
CC       oligopeptide-|-Xaa-Yaa, when Xaa is not Pro, and Yaa is neither
CC       Asp nor Glu. Thus, conversion of angiotensin I to angiotensin II,
CC       with increase in vasoconstrictor activity, but no action on
CC       angiotensin II.
CC   -!- COFACTOR: Binds 1 zinc ion per subunit.
CC   -!- COFACTOR: Binds 2 chloride ions per subunit.
CC   -!- ENZYME REGULATION: Strongly activated by chloride. Specifically
CC       inhibited by lisinopril, captopril and enalaprilat.
CC   -!- BIOPHYSICOCHEMICAL PROPERTIES:
CC       Kinetic parameters:
CC         KM=2.7 mM for Hip-His-Leu;
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. A soluble form
CC       released by proteolysis also exists.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Testis-specific;
CC         IsoId=P22966-1; Sequence=Displayed;
CC       Name=Somatic;
CC         IsoId=P12821-1; Sequence=External;
CC   -!- TISSUE SPECIFICITY: Spermatocytes, adult testis.
CC   -!- INDUCTION: Expression is thought to be subject to hormonal
CC       regulation by androgens.
CC   -!- PTM: Phosphorylated by CK2 on Ser-725; which allows membrane
CC       retention (By similarity).
CC   -!- MISCELLANEOUS: The glycosidase activity probably uses different
CC       active site residues than the metalloprotease activity.
CC   -!- MISCELLANEOUS: Inhibitors of ACE are commonly used to treat
CC       hypertension and cardiac dysfunction.
CC   -!- SIMILARITY: Belongs to the peptidase M2 family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M26657; AAA60611.1; -; mRNA.
DR   EMBL; X16295; CAA34362.1; -; mRNA.
DR   EMBL; AF118569; AAD28561.1; -; Genomic_DNA.
DR   PIR; S05238; S05238.
DR   PDB; 1O86; X-ray; A=68-656.
DR   PDB; 1O8A; X-ray; A=68-656.
DR   PDB; 1UZE; X-ray; A=68-656.
DR   PDB; 1UZF; X-ray; A=68-656.
DR   Ensembl; ENSG00000159640; Homo sapiens.
DR   HGNC; HGNC:2707; ACE.
DR   MIM; 106180; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0004246; F:peptidyl-dipeptidase A activity; TAS.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR001548; Peptidase_M2.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   3D-structure; Alternative splicing; Carboxypeptidase; Chloride;
KW   Glycoprotein; Glycosidase; Hydrolase; Metal-binding; Metalloprotease;
KW   Phosphorylation; Polymorphism; Protease; Signal; Testis;
KW   Transmembrane; Zinc.
FT   SIGNAL       1     31
FT   CHAIN       32    732       Angiotensin-converting enzyme, testis-
FT                                 specific isoform.
FT   CHAIN       32    658       Angiotensin-converting enzyme, testis-
FT                                 specific isoform, soluble form.
FT   PROPEP     659    732       Removed in secreted form.
FT   TOPO_DOM    32    684       Extracellular (Potential).
FT   TRANSMEM   685    701       Potential.
FT   TOPO_DOM   702    732       Cytoplasmic (Potential).
FT   ACT_SITE   415    415
FT   ACT_SITE   457    457       Potential.
FT   METAL      414    414       Zinc (catalytic).
FT   METAL      418    418       Zinc (catalytic).
FT   METAL      442    442       Zinc (catalytic).
FT   BINDING    217    217       Chloride 1.
FT   BINDING    255    255       Chloride 2.
FT   BINDING    516    516       Chloride 1.
FT   BINDING    520    520       Chloride 1.
FT   BINDING    553    553       Chloride 2.
FT   SITE       651    651       Not glycosylated.
FT   MOD_RES    725    725       Phosphoserine (By similarity).
FT   CARBOHYD   103    103       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   121    121       N-linked (GlcNAc. . .) (complex).
FT   CARBOHYD   140    140       N-linked (GlcNAc. . .) (complex).
FT   CARBOHYD   186    186       N-linked (GlcNAc. . .) (partial).
FT   CARBOHYD   368    368       N-linked (GlcNAc. . .) (partial).
FT   CARBOHYD   617    617       N-linked (GlcNAc. . .) (partial).
FT   DISULFID   183    189
FT   DISULFID   383    401
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FT   DISULFID    569    581
FT   VARIANT      32     32       S -> P (in dbSNP:4317).
FT                                /FTId=VAR_011710.
FT   VARIANT      49     49       S -> G (in dbSNP:4318).
FT                                /FTId=VAR_011711.
FT   VARIANT     342    342       T -> M (in dbSNP:3730043).
FT                                /FTId=VAR_023435.
FT   VARIANT     444    444       I -> T (in dbSNP:4976).
FT                                /FTId=VAR_014738.
FT   VARIANT     477    477       F -> V (in dbSNP:4977).
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Query Match 41.3%; Score 1335; DB 1; Length 732;
Best Local Similarity 41.9%; Pred. No. 9.4e-86;
Matches 254; Conservative 116; Mismatches 202; Indels 34; Gaps 9;

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Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE--------NVQNMNNAGDKWSA 53
              | | :|  |:::::  :: :: : : |:||||||| |         |:|  |:
Db         70 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT------ 123

Qy         54 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 113
                :  | |: : : ::|| |:|  :: :|    : |   : :  | ||  | | ||
Db        124 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 181

Qy        114 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 173
              ||:|:    || ||| |  :|| |  | : ||||| || : |: :   | :|| | |: |
Db        182 VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 239

Qy        174 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 233
              | | | | || ||  ||   ::          :|:|  |:|::||| :||||||  |
Db        240 RLNGYVDAGDSWRSMYETPSLE----------QDLERLFQELQPLYLNLHAYVRRALHRH 289

Qy        234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 292
              |   :|:  | :||||||:|| : |:|:| | |||   |::| |:||: | |  :|:|||
Db        290 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 349

Qy        293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
              |: || |:||  :   ||  |||  | : :: ||| :|||   | ||||  || | ::|
Db        350 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 409

Qy        352 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
              : |||||||||| | |   |  || ||| |||||:|::::|| :||||| |: ||| :
Db        410 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 469

Qy        412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
              | | :||||:| ||  :  :||:|::::||| || | | |: : ::|| :: :  |:
Db        470 SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 528

Qy        472 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 531
              |||  :   || : ||: :   :|||:   : |||| ||||||| | ||||||||  | |
Db        529 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 588

Qy        532 AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 588
              |||:|   ::|| | ||  |:: : |  ||:   :|:||:||  ||: :|:     :||
Db        589 AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 648

Qy        589 STDWSP 594
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Db        649 QYNWTP 654
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RESULT 12
Q8N710_HUMAN
ID   Q8N710_HUMAN PRELIMINARY;      PRT;   739 AA.
AC   Q8N710;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Angiotensin I converting enzyme, isoform 3.
GN   Name=ACE;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RA   Director MGC Project;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC036375; AAH36375.1; -; mRNA.
DR   HSSP; Q10714; 1J37.
DR   SMR; Q8N710; 71-648.
DR   Ensembl; ENSG00000159640; Homo sapiens.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001548; Peptidase_M2.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   739 AA;  83958 MW;  87995DFF58D93D01 CRC64;
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Query Match 41.3%; Score 1335; DB 2; Length 739;
Best Local Similarity 41.9%; Pred. No. 9.5e-86;
Matches 254; Conservative 116; Mismatches 202; Indels 34; Gaps 9;

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Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE--------NVQNMNNAGDKWSA 53
              | | :|  |:::::  :: :: : : |:||||||| |         |:|  |:
Db         70 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT------ 123

Qy         54 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 113
                :  | |: : : ::|| |:|  :: :|    : |   : :  | ||  | | ||
Db        124 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 181

Qy        114 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 173
              ||:|:    || ||| |  :|| |  | : ||||| || : |: :   | :|| | |: |
Db        182 VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 239

Qy        174 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 233
              | | | | || ||  ||   ::          :|:|  |:|::||| :||||||  |
Db        240 RLNGYVDAGDSWRSMYETPSLE----------QDLERLFQELQPLYLNLHAYVRRALHRH 289

Qy        234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 292
              |   :|:  | :||||||:|| : |:|:| | |||   |::| |:||: | |  :|:|||
Db        290 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 349

Qy        293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
              |: || |:||  :   ||  |||  | : :: ||| :|||   | ||||  || | ::|
Db        350 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 409
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Qy        352 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
              : |||||||||| | |   |  || ||| |||||:|::::|| :||||| |: ||| :
Db        410 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 469

Qy        412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
              | | :||||:| ||  :  :||:|::::||| || | | |: : ::|| :: :  |:
Db        470 SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 528

Qy        472 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 531
              |||  :   || : ||: :   :|||:   : |||| ||||||| | ||||||||  | |
Db        529 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 588

Qy        532 AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 588
              |||:|   ::|| | ||  |:: : |  ||:   :|:||:||  ||: :|:     :||
Db        589 AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 648

Qy        589 STDWSP 594
                :|:|
Db        649 QYNWTP 654
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RESULT 13
ACE_HUMAN
ID   ACE_HUMAN      STANDARD;      PRT;  1306 AA.
AC   P12821; Q53YX9; Q59GY8;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
DE   (Dipeptidyl carboxypeptidase I) (Kininase II) (CD143 antigen)
DE   [Contains: Angiotensin-converting enzyme, somatic isoform, soluble
DE   form].
GN   Name=ACE; Synonyms=DCP, DCP1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=89071703; PubMed=2849100;
RA   Soubrier F., Alhenc-Gelas F., Hubert C., Allegrini J., John M.,
RA   Tregear G., Corbol P.;
RT   "Two putative active centers in human angiotensin I-converting enzyme
RT   revealed by molecular cloning.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:9386-9390(1988).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS SER-261; TRP-561 AND
RP   SER-1286.
RX   MEDLINE=99251580; PubMed=10319862; DOI=10.1038/8760;
RA   Rieder M.J., Taylor S.L., Clark A.G., Nickerson D.A.;
RT   "Sequence variation in the human angiotensin converting enzyme.";
RL   Nat. Genet. 22:59-62(1999).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1-1239.
RC   TISSUE=Brain;
RA   Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA   Ohara O., Nagase T., Kikuno F.R.;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   PARTIAL PROTEIN SEQUENCE OF 30-46.
RC   TISSUE=Lung;
RX   MEDLINE=90110025; PubMed=2558109;
RA   Takeuchi K., Shimizu T., Ohishi N., Seyama Y., Takaku F.,
RA   Yotsumoto H.;
RT   "Purification of human lung angiotensin-converting enzyme by high-
RT   performance liquid chromatography: properties and N-terminal amino
RT   acid sequence.";
RL   J. Biochem. 106:442-445(1989).
RN   [5]
RP   ZINC-BINDING.
RX   MEDLINE=91308093; PubMed=1649623;
RA   Ehlers M.R.W., Riordan J.F.;
RT   "Angiotensin-converting enzyme: zinc- and inhibitor-binding
RT   stoichiometries of the somatic and testis isozymes.";
RL   Biochemistry 30:7118-7126(1991).
RN   [6]
RP   CARBOHYDRATE-LINKAGE SITES ASN-38; ASN-54; ASN-111; ASN-146; ASN-509
RP   AND ASN-942, AND MASS SPECTROMETRY.
RX   PubMed=9013598;
RA   Yu X.C., Sturrock E.D., Wu Z., Biemann K., Ehlers M.R.W.,
RA   Riordan J.F.;
RT   "Identification of N-linked glycosylation sites in human testis
RT   angiotensin-converting enzyme and expression of an active
RT   deglycosylated form.";
RL   J. Biol. Chem. 272:3511-3519(1997).
RN   [7]
RP   CLEAVAGE SITE, AND MASS SPECTROMETRY.
RX   PubMed=10769174;
RA   Woodman Z.L., Oppong S.Y., Cook S., Hooper N.M., Schwager S.L.U.,
RA   Brandt W.F., Ehlers M.R.W., Sturrock E.D.;
RT   "Shedding of somatic angiotensin-converting enzyme (ACE) is
RT   inefficient compared with testis ACE despite cleavage at identical
RT   stalk sites.";
RL   Biochem. J. 347:711-718(2000).
RN   [8]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=20429895; PubMed=10969042;
RA   Donoghue M., Hsieh F., Baronas E., Godbout K., Gosselin M.,
RA   Stagliano N., Donovan M., Woolf B., Robison K., Jeyaseelan R.,
RA   Breitbart R.E., Acton S.;
RT   "A novel angiotensin-converting enzyme-related carboxypeptidase (ACE2)
RT   converts angiotensin I to angiotensin 1-9.";
RL   Circ. Res. 87:E1-E9(2000).
RN   [9]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=20517872; PubMed=10924499; DOI=10.1074/jbc.M002615200;
RA   Tipnis S.R., Hooper N.M., Hyde R., Karran E., Christie G.,
RA   Turner A.J.;
RT   "A human homolog of angiotensin-converting enzyme. Cloning and
RT   functional expression as a captopril-insensitive carboxypeptidase.";
RL   J. Biol. Chem. 275:33238-33243(2000).
RN   [10]
RP   BIOPHYSICOCHEMICAL PROPERTIES, AND CHARACTERIZATION OF VARIANT
RP   LEU-1228.
RX   PubMed=11076943; DOI=10.1074/jbc.M007706200;
RA   Eyries M., Michaud A., Deinum J., Agrapart M., Chomilier J.,
RA   Kramers C., Soubrier F.;
RT   "Increased shedding of angiotensin-converting enzyme by a mutation
RT   identified in the stalk region.";
RL   J. Biol. Chem. 276:5525-5532(2001).
RN   [11]
RP   PHOSPHORYLATION SITE SER-1299, AND MUTAGENESIS OF SER-1299.
RX   PubMed=12386153;
RA   Kohlstedt K., Shoghi F., Mueller-Esterl W., Busse R., Fleming I.;
RT   "CK2 phosphorylates the angiotensin-converting enzyme and regulates
RT   its retention in the endothelial cell plasma membrane.";
RL   Circ. Res. 91:749-756(2002).
RN   [12]
RP   TISSUE SPECIFICITY.
RX   PubMed=12459472;
RA   Harmer D., Gilbert M., Borman R., Clark K.L.;
RT   "Quantitative mRNA expression profiling of ACE 2, a novel homologue of
RT   angiotensin converting enzyme.";
RL   FEBS Lett. 532:107-110(2002).
RN   [13]
RP   INDUCTION.
RX   PubMed=15151696; DOI=10.1186/1741-7015-2-19;
RA   Goulter A.B., Goddard M.J., Allen J.C., Clark K.L.;
RT   "ACE2 gene expression is up-regulated in the human failing heart.";
RL   BMC Med. 2:19-19(2004).
RN   [14]
RP   TISSUE SPECIFICITY, AND INDUCTION.
RX   PubMed=15671045; DOI=10.1093/eurheartj/ehi114;
RA   Burrell L.M., Risvanis J., Kubota E., Dean R.G., MacDonald P.S.,
RA   Lu S., Tikellis C., Grant S.L., Lew R.A., Smith A.I., Cooper M.E.,
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RA   Johnston C.I.;
RT   "Myocardial infarction increases ACE2 expression in rat and humans.";
RL   Eur. Heart J. 26:369-375(2005).
RN   [15]
RP   VARIANTS THR-1018; VAL-1051; GLN-1279; SER-1286 AND PRO-1296.
RX   MEDLINE=99318094; PubMed=10391210; DOI=10.1038/10297;
RA   Halushka M.K., Fan J.-B., Bentley K., Hsie L., Shen N., Weder A.,
RA   Cooper R., Lipshutz R., Chakravarti A.;
RT   "Patterns of single-nucleotide polymorphisms in candidate genes for
RT   blood-pressure homeostasis.";
RL   Nat. Genet. 22:239-247(1999).
CC   -!- FUNCTION: Converts angiotensin I to angiotensin II by release of
CC       the terminal His-Leu, this results in an increase of the
CC       vasoconstrictor activity of angiotensin. Also able to inactivate
CC       bradykinin, a potent vasodilator.
CC   -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
CC       oligopeptide-|-Xaa-Yaa, when Xaa is not Pro, and Yaa is neither
CC       Asp nor Glu. Thus, conversion of angiotensin I to angiotensin II,
CC       with increase in vasoconstrictor activity, but no action on
CC       angiotensin II.
CC   -!- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
CC   -!- COFACTOR: Binds 2 chloride ions per subunit (By similarity).
CC   -!- ENZYME REGULATION: Strongly activated by chloride. Specifically
CC       inhibited by lisinopril, captopril and enalaprilat.
CC   -!- BIOPHYSICOCHEMICAL PROPERTIES:
CC       Kinetic parameters:
CC         KM=2.51 mM for Hip-His-Leu;
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. A soluble form
CC       released by proteolysis also exists.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Somatic;
CC         IsoId=P12821-1; Sequence=Displayed;
CC       Name=Testis-specific;
CC         IsoId=P22966-1; Sequence=External;
CC   -!- TISSUE SPECIFICITY: Ubiquitously expressed, with highest levels in
CC       lung, kidney, heart, gastrointestinal system and prostate.
CC   -!- INDUCTION: Up-regulated in failing heart.
CC   -!- PTM: Phosphorylated by CK2 on Ser-1299; which allows membrane
CC       retention.
CC   -!- MISCELLANEOUS: Inhibitors of ACE are commonly used to treat
CC       hypertension and some types of renal and cardiac dysfunction.
CC   -!- SIMILARITY: Belongs to the peptidase M2 family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; J04144; AAA51684.1; -; mRNA.
DR   EMBL; AF118569; AAD28560.1; -; Genomic_DNA.
DR   EMBL; AY436326; AAR03504.1; -; Genomic_DNA.
DR   EMBL; AB208971; BAD92208.1; ALT_INIT; mRNA.
DR   PIR; A31759; A31759.
DR   HSSP; Q10714; 1J36.
DR   SMR; P12821; 645-1222.
DR   MEROPS; M02.001; -.
DR   MEROPS; M02.004; -.
DR   Ensembl; ENSG00000159640; Homo sapiens.
DR   HGNC; HGNC:2707; ACE.
DR   MIM; 106180; -.
DR   GO; GO:0005624; C:membrane fraction; TAS.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0008217; P:regulation of blood pressure; TAS.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR001548; Peptidase_M2.
DR   Pfam; PF01401; Peptidase_M2; 2.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 2.
DR   PROSITE; PS00142; ZINC_PROTEASE; 2.
KW   Alternative splicing; Carboxypeptidase; Direct protein sequencing;
KW   Glycoprotein; Hydrolase; Metal-binding; Metalloprotease;
KW   Phosphorylation; Polymorphism; Protease; Repeat; Signal;
KW   Transmembrane; Zinc.
FT   SIGNAL       1     29

  Query Match             41.3%;  Score 1335;  DB 1;  Length 1306;
  Best Local Similarity   41.9%;  Pred. No. 2.1e-85;
  Matches  254;  Conservative  116;  Mismatches  202;  Indels   34;  Gaps    9;

Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE--------NVQNMNNAGDKWSA 53
              | | :|  |:::::  :: :: : : |:|||||||| |         |:|  |:
Db        644 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT------ 697

Qy         54 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 113
                :  | |: : : ::|| |:|  :: :|   : |  : :  | ||  | | ||
Db        698 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 755

Qy        114 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 173
              ||:|:    || ||| |  :|| |  | : ||||| || : |: :   | :|| | |: |
Db        756 VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 813

Qy        174 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 233
              | | | || ||  ||   ::          :|:|  |:|::||| :|||||  |
Db        814 RLNGYVDAGDSWRSMYETPSLE----------QDLERLFQELQPLYLNLHAYVRRALHRH 863

Qy        234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 292
              |   :|:  | :||||||:|| : |:|:| | |||   |::| |:||: | |  :|:|||
Db        864 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 923

Qy        293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
              |: || |:||  :   ||  |||  | : :: ||| :|||   | ||||  || | ::|
Db        924 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 983

Qy        352 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
              : |||||||||| | |   |  || ||| |||||:|::::|| :|||||  |: ||| :
Db        984 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 1043

Qy        412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
              | | :||||:| ||  :  :||:|::::||| || | | |: : ::|| :: :  |:
Db       1044 SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 1102

Qy        472 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 531
              |||  :   || : ||: :   :|||:   : |||| |||||||| | |||||||  | |
Db       1103 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 1162

Qy        532 AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 588
              |||:|   ::|| | ||  |:: : |  ||:   :|:||:||  ||: :|:     :||
Db       1163 AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 1222

Qy        589 STDWSP 594
                :|:|
Db       1223 QYNWTP 1228


RESULT 14
ACET_MOUSE
ID   ACET_MOUSE     STANDARD;      PRT;   732 AA.
AC   P22967;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Angiotensin-converting enzyme, testis-specific isoform precursor
DE   (EC 3.4.15.1) (EC 3.2.1.-) (ACE-T) (Dipeptidyl carboxypeptidase I)
DE   (Kininase II) [Contains: Angiotensin-converting enzyme, testis-
DE   specific isoform, soluble form].
GN   Name=Ace; Synonyms=Dcp1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
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RX   MEDLINE=90318396; PubMed=2164636;
RA   Howard T.E., Shai S.-Y., Langford K.G., Martin B.M., Bernstein K.E.;
RT   "Transcription of testicular angiotensin-converting enzyme (ACE) is
RT   initiated within the 12th intron of the somatic ACE gene.";
RL   Mol. Cell. Biol. 10:4294-4302(1990).
RN   [2]
RP   FUNCTION.
RX   PubMed=7753170; DOI=10.1038/375146a0;
RA   Krege J.H., John S.W., Langenbach L.L., Hodgin J.B., Hagaman J.R.,
RA   Bachman E.S., Jennette J.C., O'Brien D.A., Smithies O.;
RT   "Male-female differences in fertility and blood pressure in ACE-
RT   deficient mice.";
RL   Nature 375:146-148(1995).
RN   [3]
RP   FUNCTION.
RX   PubMed=8642790;
RA   Esther C.R. Jr., Howard T.E., Marino E.M., Goddard J.M.,
RA   Capecchi M.R., Bernstein K.E.;
RT   "Mice lacking angiotensin-converting enzyme have low blood pressure,
RT   renal pathology, and reduced male fertility.";
RL   Lab. Invest. 74:953-965(1996).
RN   [4]
RP   FUNCTION, ENZYME REGULATION, AND MUTAGENESIS OF HIS-413; GLU-414 AND
RP   HIS-417.
RX   PubMed=15665832; DOI=10.1038/nm1179;
RA   Kondoh G., Tojo H., Nakatani Y., Komazawa N., Murata C., Yamagata K.,
RA   Maeda Y., Kinoshita T., Okabe M., Taguchi R., Takeda J.;
RT   "Angiotensin-converting enzyme is a GPI-anchored protein releasing
RT   factor crucial for fertilization.";
RL   Nat. Med. 11:160-166(2005).
CC   -!- FUNCTION: Converts angiotensin I to angiotensin II by release of
CC       the terminal His-Leu, this results in an increase of the
CC       vasoconstrictor activity of angiotensin. Also able to inactivate
CC       bradykinin, a potent vasodilator. Has also a glycosidase activity
CC       which releases GPI-anchored proteins from the membrane by cleaving
CC       the mannose linkage in the GPI moiety. This GPIase activity seems
CC       to be crucial for the egg-binding ability of the sperm.
CC   -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
CC       oligopeptide-|-Xaa-Yaa, when Xaa is not Pro, and Yaa is neither
CC       Asp nor Glu. Thus, conversion of angiotensin I to angiotensin II,
CC       with increase in vasoconstrictor activity, but no action on
CC       angiotensin II.
CC   -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC   -!- COFACTOR: Binds 2 chloride ions per subunit (By similarity).
CC   -!- ENZYME REGULATION: Peptidase activity is specifically inhibited by
CC       lisinopril, captopril and enalaprilat. In contrast, GPIase
CC       activity is nearly insensitive to captopril.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. A soluble form
CC       released by proteolysis also exists (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Testis-specific;
CC         IsoId=P22967-1; Sequence=Displayed;
CC       Name=Somatic;
CC         IsoId=P09470-1; Sequence=External;
CC   -!- TISSUE SPECIFICITY: Spermatocytes, adult testis.
CC   -!- INDUCTION: Expression is thought to be subject to hormonal
CC       regulation by androgens.
CC   -!- PTM: Phosphorylated by CK2 on Ser-725; which allows membrane
CC       retention (By similarity).
CC   -!- MISCELLANEOUS: Mice lacking ACE have low blood pressure, elevated
CC       serum potassium, anemia, and renal defects. Male mice have reduced
CC       fertility.
CC   -!- SIMILARITY: Belongs to the peptidase M2 family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M55333; AAA37149.1; -; mRNA.
DR   EMBL; M61094; AAA37150.1; -; Genomic_DNA.
DR   PIR; A35655; A35655.
DR   HSSP; Q10714; 1J36.
DR   SMR; P22967; 70-647.
DR   Ensembl; ENSMUSG00000020681; Mus musculus.
DR   MGI; MGI:87874; Ace.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR001548; Peptidase_M2.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Alternative splicing; Carboxypeptidase; Chloride; Glycoprotein;
KW   Glycosidase; Hydrolase; Metal-binding; Metalloprotease;
KW   Phosphorylation; Protease; Signal; Testis; Transmembrane; Zinc.
FT   SIGNAL        1     31       By similarity.
FT   CHAIN        32    732       Angiotensin-converting enzyme, testis-
FT                                 specific isoform.
FT   CHAIN        32    657       Angiotensin-converting enzyme, testis-
FT                                 specific isoform, soluble form.
FT   PROPEP      658    732       Removed in secreted form (By similarity).
FT   TOPO_DOM     32    684       Extracellular (Potential).
FT   TRANSMEM    685    701       Potential.
FT   TOPO_DOM    702    732       Cytoplasmic (Potential).
FT   ACT_SITE    414    414
FT   ACT_SITE    456    456       Potential.
FT   METAL       413    413       Zinc (catalytic) (By similarity).
FT   METAL       417    417       Zinc (catalytic) (By similarity).
FT   METAL       441    441       Zinc (catalytic) (By similarity).
FT   BINDING     216    216       Chloride 1 (By similarity).
FT   BINDING     254    254       Chloride 2 (By similarity).
FT   BINDING     515    515       Chloride 1 (By similarity).
FT   BINDING     519    519       Chloride 1 (By similarity).
FT   BINDING     552    552       Chloride 2 (By similarity).
FT   MOD_RES     725    725       Phosphoserine (By similarity).
FT   CARBOHYD    102    102       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    120    120       N-linked (GlcNAc. . .) (complex) (By
FT                                 similarity).
FT   CARBOHYD    139    139       N-linked (GlcNAc. . .) (complex) (By
FT                                 similarity).
FT   CARBOHYD    185    185       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    367    367       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    616    616       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    182    188       By similarity.
FT   DISULFID    382    400       By similarity.
FT   DISULFID    568    580       By similarity.
FT   MUTAGEN     413    413       H->K: Abolishes peptidase activity but no
FT                                 effect on GPIase activity; when
FT                                 associated to K-417.
FT   MUTAGEN     414    414       E->D: Abolishes peptidase activity but no
FT                                 effect on GPIase activity.
FT   MUTAGEN     417    417       H->K: Abolishes peptidase activity but no
FT                                 effect on GPIase activity; when
FT                                 associated to K-413.
SQ   SEQUENCE   732 AA;  84047 MW;  16C817E7FBD09BD9 CRC64;

  Query Match             41.3%;  Score 1334;  DB 1;  Length 732;
  Best Local Similarity   42.6%;  Pred. No. 1.1e-85;
  Matches  255;  Conservative  112;  Mismatches  213;  Indels   18;  Gaps    7;

Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 61
              | | :|  |:::::  |: |  : : |:| |||||| |  : :     : |    :  |
Db         69 TDEAKADRFVEEYDRTAQVLLNEYAEANWQYNTNITIEGSKILLEKSTEVSNHTLKYGTR 128

Qy         62 AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 121
                |: : :   || ::|  :: ||    :||   : :  | ||  | | ||   :|  :
Db        129 AKTFDVSNFQNSSIKRIIKKLQNLDRAVLPPKELEEYNQILLDMETTYSLSNICYTNG-- 186

Qy        122 ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 181
               |: ||| |  :|| |  | | ||||:||| :||: : | : :||   |::|: | | |
Db        187 TCMPLEPDLTNMMATSRKYEELLWAWKSWRDKVGRAILPFFPKYVEFSNKIAKLNGYTDA 246
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Qy        182 GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 240
              || ||  || : ::           :|:|  ::|::||| :|||||  |    | | ||:
Db        247 GDSWRSLYESDNLE----------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 296

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
               | :||||||:|| : |:|:| |  ||   |||| |:||: | |  :||||||: || |:
Db        297 DGPIPAHLLGNMWAQTWSNIYDLVAPFPSAPNIDATEAMIKQGWTPRRIFKEADNFFTSL 356

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG 359
              ||  :   ||  |||  | : ::  ||||:|||   | ||||  || | |:| : ||||||
Db        357 GLLPVPPEFWNKSMLEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMG 416

Qy        360 HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 419
              ||||  |  |    |  ||| |||||:|:||:|| :||||| |: ||| :     | :||
Db        417 HIQYFMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN 475

Qy        420 FLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 479
              ||:| ||  :  :||:|::::||| || | | |: : ::|| :: :  |:  |||  :
Db        476 FLMKMALDKIAFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGD 535

Qy        480 CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM 539
              || | |||  :  ::||:   : |||| ||||:|| | ||||||||  | |||: | :
Db        536 FDPGSKFHVPANVPYVRYFVSFIIQFQFHEALCRAAGHTGPLHKCDIYQSKEAGKLLADA 595

Qy        540 LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 594
              ::|| |:||  |:: : |  ||:   ::|||:||  ||  :|:     :||  :|:|
Db        596 MKLGYSKPWPEAMKLITGQPNMSASAMMNYFKPLTEWLVTENRRHGETLGWPEYNWAP 653


RESULT 15
Q8K233_MOUSE
ID   Q8K233_MOUSE PRELIMINARY;      PRT;  1015 AA.
AC   Q8K233;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Ace protein (Fragment).
GN   Name=Ace;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034367; AAH34367.1; -; mRNA.
DR   HSSP; Q10714; 1J37.
DR   SMR; Q8K233; 416-993.
DR   MGI; MGI:87874; Ace.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   InterPro; IPR001548; Peptidase_M2.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   Pfam; PF01401; Peptidase_M2; 2.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 2.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_2.
FT   NON_TER      1      1
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  Query Match             41.3%;  Score 1334;  DB 2;  Length 1015;
  Best Local Similarity   42.6%;  Pred. No. 1.7e-85;
  Matches  255;  Conservative  112;  Mismatches  213;  Indels   18;  Gaps    7;

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Qy         62 AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 121
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Qy        122 ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 181
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Db        533 TCMPLEPDLTNMMATSRKYEELLWAWKSWRDKVGRAILPFFPKYVEFSNKIAKLNGYTDA 592

Qy        182 GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 240
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Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
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Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG 359
              ||  :   ||  |||  | : ::  ||||:|||   | ||||  || | |:| : ||||||
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Db        822 FLMKMALDKIAFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGD 881

Qy        480 CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM 539
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Job time : 126.785 secs
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OM protein - protein search, using sw model

Run on: March 28, 2006, 11:36:19 ; Search time 95.1865 Seconds
(without alignments)
2611.802 Million cell updates/sec

Title: US-10-659-000-4
Perfect score: 3231
Sequence: 1 STIEEQAKTFLDKFNHEAED.....WLKDQNKNSFVGWSTDWSPY 595

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 3231 | 100.0 | 595 | 4 | US-10-659-000-4 | Sequence 4, Appli |
| 2 | 3231 | 100.0 | 805 | 3 | US-09-978-385-2 | Sequence 2, Appli |
| 3 | 3231 | 100.0 | 805 | 3 | US-09-999-781-2 | Sequence 2, Appli |
| 4 | 3231 | 100.0 | 805 | 4 | US-10-158-847-142 | Sequence 142, App |
| 5 | 3231 | 100.0 | 805 | 4 | US-10-005-956-570 | Sequence 570, App |
| 6 | 3231 | 100.0 | 805 | 4 | US-10-005-956-843 | Sequence 843, App |
| 7 | 3231 | 100.0 | 805 | 4 | US-10-158-825-142 | Sequence 142, App |
| 8 | 3231 | 100.0 | 805 | 4 | US-10-158-825-142 | Sequence 142, App |
| 9 | 3231 | 100.0 | 805 | 5 | US-10-756-149-5456 | Sequence 5456, Ap |
| 10 | 3231 | 100.0 | 805 | 6 | US-11-059-218-2 | Sequence 2, Appli |
| 11 | 3231 | 100.0 | 805 | 6 | US-11-059-218-106 | Sequence 106, App |
| 12 | 3227 | 99.9 | 805 | 4 | US-10-114-893-86 | Sequence 86, Appl |
| 13 | 2987 | 92.4 | 681 | 3 | US-09-969-384-25 | Sequence 25, Appl |
| 14 | 2987 | 92.4 | 681 | 4 | US-10-158-847-140 | Sequence 140, App |
| 15 | 2987 | 92.4 | 681 | 4 | US-10-158-825-140 | Sequence 140, App |
| 16 | 2987 | 92.4 | 681 | 4 | US-10-158-825-140 | Sequence 140, App |
| 17 | 2987 | 92.4 | 711 | 3 | US-09-969-384-13 | Sequence 13, Appl |
| 18 | 2987 | 92.4 | 711 | 4 | US-10-158-847-138 | Sequence 138, App |
| 19 | 2987 | 92.4 | 711 | 4 | US-10-158-825-138 | Sequence 138, App |
| 20 | 2987 | 92.4 | 711 | 4 | US-10-158-825-138 | Sequence 138, App |
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| 22 | 2897 | 89.7 | 555 | 4 | US-10-140-808-72 | Sequence 72, Appl |
| 23 | 2897 | 89.7 | 555 | 4 | US-10-121-049-72 | Sequence 72, Appl |
| 24 | 2897 | 89.7 | 555 | 4 | US-10-123-904-72 | Sequence 72, Appl |
| 25 | 2897 | 89.7 | 555 | 4 | US-10-140-470-72 | Sequence 72, Appl |
| 26 | 2897 | 89.7 | 555 | 4 | US-10-175-746-72 | Sequence 72, Appl |
| 27 | 2897 | 89.7 | 555 | 4 | US-10-176-918-72 | Sequence 72, Appl |
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| 36 | 2897 | 89.7 | 555 | 4 | US-10-121-050-72 | Sequence 72, Appl |
| 37 | 2897 | 89.7 | 555 | 4 | US-10-141-755-72 | Sequence 72, Appl |
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| 41 | 2897 | 89.7 | 555 | 4 | US-10-123-261-72 | Sequence 72, Appl |
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| 43 | 2897 | 89.7 | 555 | 4 | US-10-140-928-72 | Sequence 72, Appl |
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| 45 | 2897 | 89.7 | 555 | 4 | US-10-123-292-72 | Sequence 72, Appl |

ALIGNMENTS

RESULT 1
US-10-659-000-4
; Sequence 4, Application US/10659000
; Publication No. US20040209344A1
; GENERAL INFORMATION:
; APPLICANT: PANTOLIANO, MICHAEL W.
; APPLICANT: RYAN, M. DOMINIC
; APPLICANT: STAKER, BART LEE
; APPLICANT: PRASAD, G. SRIDHAR
; APPLICANT: TANG, JIN
; APPLICANT: MENON, SAURABH PRABHAKAR
; APPLICANT: TOWLER, PAUL S.
; APPLICANT: WILLIAMS, DAVID H.
; APPLICANT: FISHER, MARTIN
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ANGIOTENSIN-CONVERTING ENZYME-RELATED
; TITLE OF INVENTION: CARBOXYPEPTIDASE
; FILE REFERENCE: MNM/002
; CURRENT APPLICATION NUMBER: US/10/659,000
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/410,010
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-000-4

Query Match 100.0%; Score 3231; DB 4; Length 595;
Best Local Similarity 100.0%; Pred. No. 1.5e-273;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
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Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
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RESULT 2
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; Sequence 2, Application US/09978385
; Patent No. US20020177211A1
; GENERAL INFORMATION:
;  APPLICANT: Piddington, Christopher S.
;  APPLICANT:  Petrie, Charles
;  APPLICANT:  Shoemaker, Kimberly E.
;  APPLICANT:  Bishop, Paul D.
;  TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
;  FILE REFERENCE: 99-24C1
;  CURRENT APPLICATION NUMBER: US/09/978,385
;  CURRENT FILING DATE:  2001-10-16
;  PRIOR APPLICATION NUMBER: 60/133,952
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/151,181
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: 09/563,516
;  PRIOR FILING DATE: 2000-05-03
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-978-385-2

  Query Match           100.0%;  Score 3231;  DB 3;  Length 805;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-273;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

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Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360

Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

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Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

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; Sequence 2, Application US/09999781
; Publication No. US20040082496A1
; GENERAL INFORMATION:
;  APPLICANT: ACTON, SUSAN L.
;  APPLICANT:  OCAIN, TIMOTHY D.
;  APPLICANT:  GOULD, ALEXANDRA
;  APPLICANT:  DALES, NATALIE A.
;  APPLICANT:  GUAN, BING
;  APPLICANT:  BROWN,  JAMES A.
;  APPLICANT:  PATANE, MICHAEL
;  APPLICANT:  KADAMBI, VIVEK J.
;  APPLICANT:  SOLOMON, MICHAEL
;  APPLICANT:  STRICKER-KRONGRAD, ALAIN
;  TITLE OF INVENTION: ACE-2 MODULATING COMPOUNDS AND METHODS
;  TITLE OF INVENTION:  OF USE THEREOF
;  FILE REFERENCE: MFI-082CP4
;  CURRENT APPLICATION NUMBER: US/09/999,781
;  CURRENT FILING DATE:  2001-10-31
;  PRIOR APPLICATION NUMBER: 09/870,382
;  PRIOR FILING DATE: 2001-05-29
;  PRIOR APPLICATION NUMBER: 09/704,216
;  PRIOR FILING DATE: 2000-11-01
;  PRIOR APPLICATION NUMBER: 60/XXX,XXX
;  PRIOR FILING DATE: 2001-10-19
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-999-781-2

  Query Match           100.0%;  Score 3231;  DB 3;  Length 805;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-273;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

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Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

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Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
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Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
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RESULT 4
US-10-158-847-142
; Sequence 142, Application US/10158847
; Publication No. US20030091557A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 805
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-142

Query Match 100.0%; Score 3231; DB 4; Length 805;
Best Local Similarity 100.0%; Pred. No. 2.4e-273;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
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RESULT 5
US-10-005-956-570
; Sequence 570, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 570
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-956-570

Query Match 100.0%; Score 3231; DB 4; Length 805;
Best Local Similarity 100.0%; Pred. No. 2.4e-273;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378
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Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613


RESULT 6
US-10-005-956-843
; Sequence 843, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
;  FILE REFERENCE: D0053NP
;  CURRENT APPLICATION NUMBER: US/10/005,956
;  CURRENT FILING DATE:  2001-12-03
;  PRIOR APPLICATION NUMBER: 60/251,015
;  PRIOR FILING DATE: 2000-12-04
;  PRIOR APPLICATION NUMBER: 60/263,678
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: 60/273,037
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 1579
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 843
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-005-956-843

  Query Match            100.0%;  Score 3231;  DB 4;  Length 805;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-273;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613


RESULT 7
US-10-158-825-142
; Sequence 142, Application US/10158825
; Publication No. US20030138894A1
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF555
;  CURRENT APPLICATION NUMBER: US/10/158,825
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/294,976
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-158-825-142

  Query Match            100.0%;  Score 3231;  DB 4;  Length 805;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-273;
  Matches  595;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558
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Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
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RESULT 8
US-10-158-825-142
; Sequence 142, Application US/10158825
; Publication No. US20040121429A9
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF555
; CURRENT APPLICATION NUMBER: US/10/158,825
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 805
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-825-142

Query Match 100.0%; Score 3231; DB 4; Length 805;
Best Local Similarity 100.0%; Pred. No. 2.4e-273;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
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RESULT 9
US-10-756-149-5456
; Sequence 5456, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5456
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5456

Query Match 100.0%; Score 3231; DB 5; Length 805;
Best Local Similarity 100.0%; Pred. No. 2.4e-273;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
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RESULT 10
US-11-059-218-2
; Sequence 2, Application US/11059218
; Publication No. US20050147600A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L. et al.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
; TITLE OF INVENTION: DIAGNOSTIC USES THEREFOR
; FILE REFERENCE: MNI-132CP3
; CURRENT APPLICATION NUMBER: US/11/059,218
; CURRENT FILING DATE: 2005-02-16

; PRIOR APPLICATION NUMBER: US/09/635,501
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 09/407,427
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/163,648
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 08/989,299
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-059-218-2

Query Match 100.0%; Score 3231; DB 6; Length 805;
Best Local Similarity 100.0%; Pred. No. 2.4e-273;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
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RESULT 11
US-11-059-218-106
; Sequence 106, Application US/11059218
; Publication No. US20050147600A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L. et al.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
; TITLE OF INVENTION: DIAGNOSTIC USES THEREFOR
; FILE REFERENCE: MNI-132CP3
; CURRENT APPLICATION NUMBER: US/11/059,218
; CURRENT FILING DATE: 2005-02-16
; PRIOR APPLICATION NUMBER: US/09/635,501
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 09/407,427
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/163,648
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 08/989,299
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-059-218-106

Query Match 100.0%; Score 3231; DB 6; Length 805;
Best Local Similarity 100.0%; Pred. No. 2.4e-273;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
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RESULT 12
US-10-114-893-86
; Sequence 86, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.

```
;  APPLICANT: Spaulding, Vikki
;  APPLICANT: Carlin-Duckett, McKeough
;  APPLICANT: Kelleher, Kerry S.
;  APPLICANT: Genetics Institute, Inc.
;  TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
;  FILE REFERENCE: GI 6000-10A
;  CURRENT APPLICATION NUMBER: US/10/114,893
;  CURRENT FILING DATE: 2002-04-02
;  EARLIER APPLICATION NUMBER: 09/413,232
;  EARLIER FILING DATE: 1999-10-06
;  NUMBER OF SEQ ID NOS: 321
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-114-893-86

  Query Match             99.9%;  Score 3227;  DB 4;  Length 805;
  Best Local Similarity   99.8%;  Pred. No. 5.4e-273;
  Matches  594;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMEDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613


RESULT 13
US-09-969-384-25
; Sequence 25, Application US/09969384
; Publication No. US20020192749A1
; GENERAL INFORMATION:
;  APPLICANT: Moore, et al.
;  TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
;  FILE REFERENCE: PT055P1
;  CURRENT APPLICATION NUMBER: US/09/969,384
;  CURRENT FILING DATE:  2001-10-03
;  PRIOR APPLICATION NUMBER: PCT/US01/10542
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: 60/236,384
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: 60/194,118
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
;   LENGTH: 681
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (219)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (240)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (499)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-969-384-25

  Query Match             92.4%;  Score 2987;  DB 3;  Length 681;
  Best Local Similarity   99.3%;  Pred. No. 4.3e-252;
  Matches  548;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         44 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 60

Qy        104 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 120

Qy        164 EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 180

Qy        224 AYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 283
              |||| |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        181 AYVRPKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYXLTVPFGQKPNIDVTDAMVDQX 240

Qy        284 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 300

Qy        344 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360

Qy        404 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 420

Qy        464 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 480

Qy        524 CDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 583
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        481 CDISNSTEAGQKLFNMLRXGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 540

Qy        584 SFVGWSTDWSPY 595
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Db        541 SFVGWSTDWSPY 552


RESULT 14
US-10-158-847-140
; Sequence 140, Application US/10158847
; Publication No. US20030091557A1
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; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF557
;  CURRENT APPLICATION NUMBER: US/10/158,847
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/295,004
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
;   LENGTH: 681
;   TYPE: PRT
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (219)..(219)
;   OTHER INFORMATION: Xaa equals any amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (240)..(240)
;   OTHER INFORMATION: Xaa equals any amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (499)..(499)
;   OTHER INFORMATION: Xaa equals any amino acid
US-10-158-847-140

  Query Match             92.4%;  Score 2987;  DB 4;  Length 681;
  Best Local Similarity   99.3%;  Pred. No. 4.3e-252;
  Matches  548;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         44 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 60

Qy        104 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 120

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Db        121 EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 180

Qy        224 AYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 283
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Qy        284 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 343
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; Sequence 140, Application US/10158825
; Publication No. US20030138894A1
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF555
;  CURRENT APPLICATION NUMBER: US/10/158,825
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/294,976
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
;   LENGTH: 681
;   TYPE: PRT
;   ORGANISM: homo sapiens
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;   NAME/KEY: MISC_FEATURE
;   LOCATION: (499)..(499)
;   OTHER INFORMATION: Xaa equals any amino acid
US-10-158-825-140

  Query Match             92.4%;  Score 2987;  DB 4;  Length 681;
  Best Local Similarity   99.3%;  Pred. No. 4.3e-252;
  Matches  548;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Qy        224 AYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 283
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Qy        524 CDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 583
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Db        481 CDISNSTEAGQKLFNMLRXGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 540

Qy        584 SFVGWSTDWSPY 595
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Db 541 SFVGWSTDWSPY 552

Search completed: March 28, 2006, 11:42:32
Job time : 97.1865 secs

GenCore version 5.1.7


OM protein - protein search, using sw model

Run on: March 28, 2006, 11:38:04 ; Search time 13.1176 Seconds
(without alignments)
1337.835 Million cell updates/sec

Title: US-10-659-000-4
Perfect score: 3231
Sequence: 1 STIEEQAKTFLDKFNHEAED.....WLKDQNKNSFVGWSTDWSPY 595

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 3231 | 100.0 | 805 | 6 | US-10-518-599-2 | Sequence 2, Appli |
| 2 | 3231 | 100.0 | 805 | 6 | US-10-957-880-1 | Sequence 1, Appli |
| 3 | 3218 | 99.6 | 702 | 6 | US-10-957-880-2 | Sequence 2, Appli |
| 4 | 2897 | 89.7 | 555 | 6 | US-10-131-826A-72 | Sequence 72, Appl |
| 5 | 2897 | 89.7 | 555 | 6 | US-10-973-115B-72 | Sequence 72, Appl |
| 6 | 2757 | 85.3 | 805 | 6 | US-10-518-599-24 | Sequence 24, Appl |
| 7 | 2755 | 85.3 | 805 | 6 | US-10-518-599-4 | Sequence 4, Appli |
| 8 | 1335 | 41.3 | 732 | 6 | US-10-518-599-23 | Sequence 23, Appl |
| 9 | 1335 | 41.3 | 732 | 6 | US-10-995-561-1020 | Sequence 1020, Ap |
| 10 | 1335 | 41.3 | 1160 | 6 | US-10-995-561-1019 | Sequence 1019, Ap |
| 11 | 1335 | 41.3 | 1302 | 6 | US-10-995-561-1024 | Sequence 1024, Ap |
| 12 | 1335 | 41.3 | 1306 | 6 | US-10-995-561-1027 | Sequence 1027, Ap |
| 13 | 1334 | 41.3 | 732 | 6 | US-10-518-599-22 | Sequence 22, Appl |
| 14 | 1269 | 39.3 | 616 | 6 | US-10-995-561-1018 | Sequence 1018, Ap |
| 15 | 1269 | 39.3 | 616 | 6 | US-10-995-561-1022 | Sequence 1022, Ap |
| 16 | 1229 | 38.0 | 638 | 6 | US-10-995-561-1025 | Sequence 1025, Ap |
| 17 | 1224 | 37.9 | 560 | 6 | US-10-995-561-1026 | Sequence 1026, Ap |
| 18 | 1125 | 34.8 | 626 | 6 | US-10-533-811-43 | Sequence 43, Appl |
| 19 | 909.5 | 28.1 | 424 | 6 | US-10-995-561-1017 | Sequence 1017, Ap |
| 20 | 433.5 | 13.4 | 254 | 6 | US-10-995-561-1021 | Sequence 1021, Ap |
| 21 | 266.5 | 8.2 | 209 | 6 | US-10-995-561-1023 | Sequence 1023, Ap |
| 22 | 122 | 3.8 | 3488 | 7 | US-11-087-099-9005 | Sequence 9005, Ap |
| 23 | 114 | 3.5 | 1493 | 6 | US-10-330-773-502 | Sequence 502, App |
| 24 | 108.5 | 3.4 | 3487 | 7 | US-11-087-099-10423 | Sequence 10423, A |
| 25 | 108 | 3.3 | 3487 | 7 | US-11-087-099-9068 | Sequence 9068, Ap |
| 26 | 106 | 3.3 | 851 | 6 | US-10-330-773-397 | Sequence 397, App |
| 27 | 104 | 3.2 | 834 | 6 | US-10-501-035-280 | Sequence 280, App |
| 28 | 99 | 3.1 | 737 | 6 | US-10-878-556A-25 | Sequence 25, Appl |
| 29 | 98 | 3.0 | 1065 | 6 | US-10-793-626-1212 | Sequence 1212, Ap |
| 30 | 96.5 | 3.0 | 349 | 6 | US-10-515-419-2 | Sequence 2, Appli |
| 31 | 96.5 | 3.0 | 349 | 6 | US-10-515-547-6 | Sequence 6, Appli |
| 32 | 96.5 | 3.0 | 352 | 6 | US-10-515-419-3 | Sequence 3, Appli |
| 33 | 94 | 2.9 | 1826 | 6 | US-10-330-773-499 | Sequence 499, App |
| 34 | 92.5 | 2.9 | 561 | 7 | US-11-029-465-12 | Sequence 12, Appl |
| 35 | 91.5 | 2.8 | 347 | 7 | US-11-087-099-6748 | Sequence 6748, Ap |
| 36 | 91 | 2.8 | 830 | 6 | US-10-330-773-404 | Sequence 404, App |
| 37 | 91 | 2.8 | 830 | 6 | US-10-330-773-406 | Sequence 406, App |
| 38 | 90.5 | 2.8 | 562 | 6 | US-10-507-928-10 | Sequence 10, Appl |
| 39 | 90.5 | 2.8 | 562 | 6 | US-10-507-928-12 | Sequence 12, Appl |
| 40 | 90.5 | 2.8 | 562 | 7 | US-11-029-465-10 | Sequence 10, Appl |
| 41 | 90.5 | 2.8 | 912 | 7 | US-11-042-988-12 | Sequence 12, Appl |
| 42 | 90 | 2.8 | 784 | 6 | US-10-517-939-324 | Sequence 324, App |
| 43 | 89.5 | 2.8 | 488 | 6 | US-10-821-234-1654 | Sequence 1654, Ap |
| 44 | 89.5 | 2.8 | 488 | 7 | US-11-186-284-121 | Sequence 121, App |
| 45 | 89.5 | 2.8 | 602 | 6 | US-10-793-626-2362 | Sequence 2362, Ap |

ALIGNMENTS

RESULT 1
US-10-518-599-2
; Sequence 2, Application US/10518599
; Publication No. US20050251873A1
; GENERAL INFORMATION:
; APPLICANT: PENNINGER, JOSEPH M.
; APPLICANT: CRACKOWER, MICHAEL A.
; TITLE OF INVENTION: ACE2 ACTIVATION FOR TREATMENT OF HEART, LUNG AND
; TITLE OF INVENTION: KIDNEY DISEASE AND HYPERTENSION
; FILE REFERENCE: SONN:064US
; CURRENT APPLICATION NUMBER: US/10/518,599
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/CA03/00882
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/389,709
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-518-599-2

Query Match 100.0%; Score 3231; DB 6; Length 805;
Best Local Similarity 100.0%; Pred. No. 1.3e-252;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
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Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

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RESULT 2
US-10-957-880-1
; Sequence 1, Application US/10957880
; Publication No. US20050282154A1
; GENERAL INFORMATION:
; APPLICANT: Brigham & Women's Hospital, Inc.
; APPLICANT: Farzan, Michael R
; APPLICANT: Li, Wenhui
; APPLICANT: Moore, Michael J
; TITLE OF INVENTION: Angiotensin-Converting Enzyme-2 as a Receptor for the SARS Corona
; FILE REFERENCE: 7570/80644
; CURRENT APPLICATION NUMBER: US/10/957,880
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-957-880-1

Query Match 100.0%; Score 3231; DB 6; Length 805;
Best Local Similarity 100.0%; Pred. No. 1.3e-252;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
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Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
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Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
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RESULT 3
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; Sequence 2, Application US/10957880
; Publication No. US20050282154A1
; GENERAL INFORMATION:
; APPLICANT: Brigham & Women's Hospital, Inc.
; APPLICANT: Farzan, Michael R
; APPLICANT: Li, Wenhui
; APPLICANT: Moore, Michael J
; TITLE OF INVENTION: Angiotensin-Converting Enzyme-2 as a Receptor for the SARS Corona
; FILE REFERENCE: 7570/80644
; CURRENT APPLICATION NUMBER: US/10/957,880
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-957-880-2

Query Match 99.6%; Score 3218; DB 6; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.2e-251;
Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        124 LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYGD 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYGD 180

Qy        184 YWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 YWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGC 240

Qy        244 LPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLP 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLP 300

Qy        304 NMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGHIQY 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGHIQY 360

Qy        364 DMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLK 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLK 420

Qy        424 QALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPA 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPA 480

Qy        484 SLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        481 SLFHVSNDYSPIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLG 540

Qy        544 KSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
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Db        541 KSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 592


RESULT 4
US-10-131-826A-72
; Sequence 72, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C128
;  CURRENT APPLICATION NUMBER: US/10/131,826A
;  CURRENT FILING DATE:  2002-04-24
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059184
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 72
;   LENGTH: 555
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-131-826A-72

  Query Match             89.7%;  Score 2897;  DB 6;  Length 555;
  Best Local Similarity   99.8%;  Pred. No. 6.7e-226;
  Matches  535;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
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Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
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Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
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Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
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Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKL 536
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Db        499 DPASLFHVSDDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKL 554


RESULT 5
US-10-973-115B-72
; Sequence 72, Application US/10973115B
; Publication No. US20060040351A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Beresini, Maureen
;  APPLICANT:  DeForge, Laura
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Gao, Wei-Quiang
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Sherwood, Steven
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODINC
;  TITLE OF INVENTION:  SAME
;  FILE REFERENCE: 39870-3330R1C300C1
;  CURRENT APPLICATION NUMBER: US/10/973,115B
;  CURRENT FILING DATE:  2004-10-22
;  PRIOR APPLICATION NUMBER: US 10/145,747
;  PRIOR FILING DATE: 2002-05-14
;  PRIOR APPLICATION NUMBER: US 10/028,072
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: US 09/581,742
;  PRIOR FILING DATE: 2000-06-16
;  PRIOR APPLICATION NUMBER: PCT/US00/05746
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 60/135,736
;  PRIOR FILING DATE: 1999-05-25
;  PRIOR APPLICATION NUMBER: US 60/123,090
;  PRIOR FILING DATE: 1999-03-05
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 72
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;   LENGTH: 555
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-973-115B-72

  Query Match            89.7%;  Score 2897;  DB 6;  Length 555;
  Best Local Similarity  99.8%;  Pred. No. 6.7e-226;
  Matches  535;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
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Db        259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
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Db        319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
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Db        379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
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Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKL 536
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Db        499 DPASLFHVSDDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKL 554


RESULT 6
US-10-518-599-24
; Sequence 24, Application US/10518599
; Publication No. US20050251873A1
; GENERAL INFORMATION:
;  APPLICANT: PENNINGER, JOSEPH M.
;  APPLICANT:  CRACKOWER, MICHAEL A.
;  TITLE OF INVENTION: ACE2 ACTIVATION FOR TREATMENT OF HEART, LUNG AND
;  TITLE OF INVENTION:  KIDNEY DISEASE AND HYPERTENSION
;  FILE REFERENCE: SONN:064US
;  CURRENT APPLICATION NUMBER: US/10/518,599
;  CURRENT FILING DATE:  2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/CA03/00882
;  PRIOR FILING DATE: 2003-06-19
;  PRIOR APPLICATION NUMBER: US 60/389,709
;  PRIOR FILING DATE: 2002-06-19
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: Rattus rattus
US-10-518-599-24

  Query Match            85.3%;  Score 2757;  DB 6;  Length 805;
  Best Local Similarity  84.2%;  Pred. No. 2.2e-214;
  Matches  501;  Conservative   42;  Mismatches   52;  Indels    0;  Gaps    0;

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Db         19 SLIEEKAESFLNKFNQEAEDLSYQSSLASWNYNTNITEENAQKMNEAAAKWSAFYEEQSK 78

Qy         61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
              :|| : |||||| |:| ||:||||:||| || ||:|:|||||||||||||||||||  ||
Db         79 IAQNFSLQEIQNATIKRQLKALQQSGSSALSPDKNKQLNTILNTMSTIYSTGKVCNSMNP 138

Qy        121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
              ||| |||||:|||| | ||| |||||| ||:|||||||||||||||||||||||:|||
Db        139 QECFLLEPGLDEIMATSTDYNRRLWAWEGWRAEVGKQLRPLYEEYVVLKNEMARANNYED 198

Qy        181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
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Db        199 YGDYWRGDYEAEGVEGYNYNRNQLIEDVENTFKEIKPLYEQLHAYVRTKLMEVYPSYISP 258

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              ||||||||||||||||||| || || ||||||||||||:|:|||:|||||||||||||||
Db        259 TGCLPAHLLGDMWGRFWTNLYPLTTPFLQKPNIDVTDAMVNQSWDAERIFKEAEKFFVSV 318

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
              ||| || ||| ||||||:||: :| ||||||||| ||||| ||||||||:||||||||||
Db        319 GLPQMTPGFWTNSMLTEPGDDRKVVCHPTAWDLGHGDFRIKMCTKVTMDNFLTAHHEMGH 378

Qy        361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
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Db        379 IQYDMAYAKQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLPSNFQEDNETEINF 438

Qy        421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
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Db        439 LLKQALTIVGTLPFTYMLEKWRWMVFQDKIPREQWTKKWWEMKREIVGVVEPLPHDETYC 498

Qy        481 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
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Db        499 DPASLFHVSNDYSFIRYYTRTIYQFQFQEALCQAAKHDGPLHKCDISNSTEAGQKLLNML 558

Qy        541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
              || | |||||||||::||:|:||||||:||| |||:||:|| ||||||||||
Db        559 SLGNSGPWTLALENVVGSRNMDVKPLLNYFQPLFVWLKEQNRNSTVGWSTDWSPY 613


RESULT 7
US-10-518-599-4
; Sequence 4, Application US/10518599
; Publication No. US20050251873A1
; GENERAL INFORMATION:
;  APPLICANT: PENNINGER, JOSEPH M.
;  APPLICANT:  CRACKOWER, MICHAEL A.
;  TITLE OF INVENTION: ACE2 ACTIVATION FOR TREATMENT OF HEART, LUNG AND
;  TITLE OF INVENTION:  KIDNEY DISEASE AND HYPERTENSION
;  FILE REFERENCE: SONN:064US
;  CURRENT APPLICATION NUMBER: US/10/518,599
;  CURRENT FILING DATE:  2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/CA03/00882
;  PRIOR FILING DATE: 2003-06-19
;  PRIOR APPLICATION NUMBER: US 60/389,709
;  PRIOR FILING DATE: 2002-06-19
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-518-599-4

  Query Match            85.3%;  Score 2755;  DB 6;  Length 805;
  Best Local Similarity  84.2%;  Pred. No. 3.2e-214;
  Matches  501;  Conservative   37;  Mismatches   57;  Indels    0;  Gaps    0;

Qy          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 60
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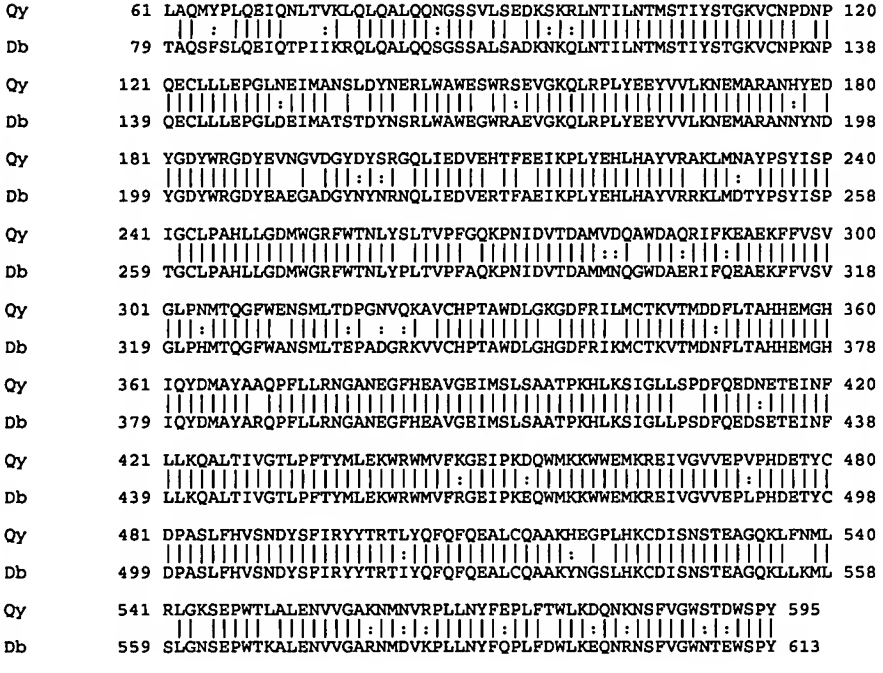
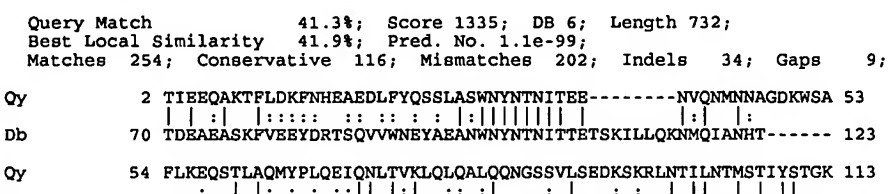
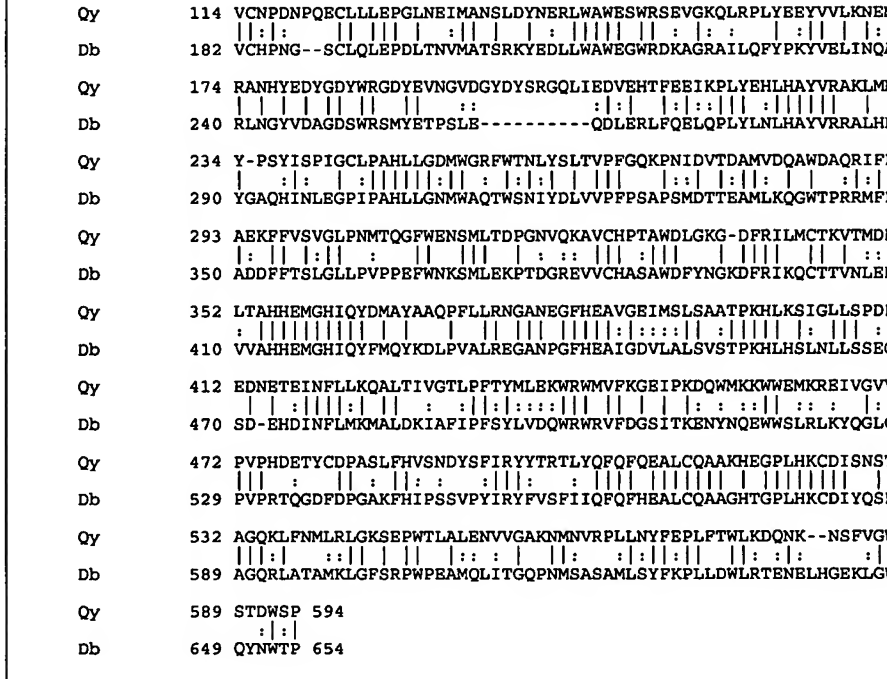


RESULT 8
US-10-518-599-23
; Sequence 23, Application US/10518599
; Publication No. US20050251873A1
; GENERAL INFORMATION:
; APPLICANT: PENNINGER, JOSEPH M.
; APPLICANT: CRACKOWER, MICHAEL A.
; TITLE OF INVENTION: ACE2 ACTIVATION FOR TREATMENT OF HEART, LUNG AND
; TITLE OF INVENTION: KIDNEY DISEASE AND HYPERTENSION
; FILE REFERENCE: SONN:064US
; CURRENT APPLICATION NUMBER: US/10/518,599
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/CA03/00882
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/389,709
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-518-599-23

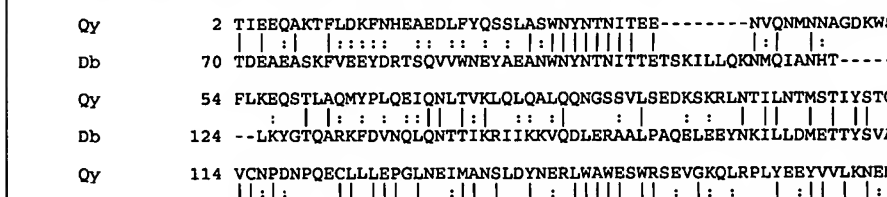
Query Match 41.3%; Score 1335; DB 6; Length 732;
Best Local Similarity 41.9%; Pred. No. 1.1e-99;
Matches 254; Conservative 116; Mismatches 202; Indels 34; Gaps 9;





RESULT 9
US-10-995-561-1020
; Sequence 1020, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1020
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1020

Query Match 41.3%; Score 1335; DB 6; Length 732;
Best Local Similarity 41.9%; Pred. No. 1.1e-99;
Matches 254; Conservative 116; Mismatches 202; Indels 34; Gaps 9;



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Qy        234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 292
Db        290 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 349

Qy        293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
Db        350 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 409

Qy        352 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
Db        410 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 469

Qy        412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
Db        470 SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 528

Qy        472 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 531
Db        529 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 588

Qy        532 AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 588
Db        589 AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 648

Qy        589 STDWSP 594
Db        649 QYNWTP 654
```

RESULT 10
US-10-995-561-1019
; Sequence 1019, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1019
; LENGTH: 1160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1019

Query Match 41.3%; Score 1335; DB 6; Length 1160;
Best Local Similarity 41.9%; Pred. No. 2e-99;
Matches 254; Conservative 116; Mismatches 202; Indels 34; Gaps 9;

```
Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE--------NVQNMNNAGDKWSA 53
Db        498 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT------ 551

Qy         54 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 113
Db        552 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 609

Qy        114 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 173
Db        610 VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 667

Qy        174 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 233
Db        668 RLNGYVDAGDSWRSMYETPSLE----------QDLERLFQELQPLYLNLHAYVRRALHRH 717

Qy        234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 292
Db        718 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 777

Qy        293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
Db        778 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 837

Qy        352 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
Db        838 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 897

Qy        412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
Db        898 SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 956

Qy        472 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 531
Db        957 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 1016

Qy        532 AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 588
Db       1017 AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 1076

Qy        589 STDWSP 594
Db       1077 QYNWTP 1082
```

RESULT 11
US-10-995-561-1024
; Sequence 1024, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1024
; LENGTH: 1302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1024

Query Match 41.3%; Score 1335; DB 6; Length 1302;
Best Local Similarity 41.9%; Pred. No. 2.3e-99;
Matches 254; Conservative 116; Mismatches 202; Indels 34; Gaps 9;

```
Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE--------NVQNMNNAGDKWSA 53
Db        640 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT------ 693

Qy         54 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 113
Db        694 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 751

Qy        114 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 173
Db        752 VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 809

Qy        174 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 233
Db        810 RLNGYVDAGDSWRSMYETPSLE----------QDLERLFQELQPLYLNLHAYVRRALHRH 859

Qy        234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 292
Db        860 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 919
```

```
Qy        293 AEKPFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
              |: || |:||  :   ||  |||  | : :: ||| :|||   | ||||  || | ::|
Db        920 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 979

Qy        352 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
              : |||||||||| | |   | || ||| ||||:|:::::|| :||||| |: ||| :
Db        980 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 1039

Qy        412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
              | | :||||:| ||  :  :||:|:::::||| || | | |: : ::|| :: :  |:
Db       1040 SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 1098

Qy        472 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 531
              |||  :   || : ||: :   :|||:   : |||| ||||||| | ||||||||  | |
Db       1099 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 1158

Qy        532 AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 588
              |||:|   ::|| | ||  |:: : |  ||:   :|:||:||  ||: :|:     :||
Db       1159 AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 1218

Qy        589 STDWSP 594
                :|:|
Db       1219 QYNWTP 1224
```

RESULT 12
US-10-995-561-1027
; Sequence 1027, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1027
; LENGTH: 1306
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1027

Query Match 41.3%; Score 1335; DB 6; Length 1306;
Best Local Similarity 41.9%; Pred. No. 2.4e-99;
Matches 254; Conservative 116; Mismatches 202; Indels 34; Gaps 9;

```
Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE--------NVQNMNNAGDKWSA 53
              | | :|  |:::::  :: :: : : |:|||||||| |        |:|  |:
Db        644 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT------ 697

Qy         54 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 113
                :  | |: : : ::|| |:|  :: :|    : |   : :  | ||  | | ||
Db        698 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 755

Qy        114 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 173
              ||:|:    || ||| |  :|| |  | : ||||| || : |: :   | :|| | |: |
Db        756 VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 813

Qy        174 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 233
              | | | | || ||  ||   ::          :|:|  |:|::||| :||||||  |
Db        814 RLNGYVDAGDSWRSMYETPSLE----------QDLERLFQELQPLYLNLHAYVRRALHRH 863

Qy        234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 292
              |  :|:  | :|||||:|| : |:|:| | |||   |::| |:||: | |  :|:|||
Db        864 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 923

Qy        293 AEKPFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
              |: || |:||  :   ||  |||  | : :: ||| :|||   | ||||  || | ::|
Db        924 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 983
```

```
Qy        352 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
              : |||||||||| | |   | || ||| |||||:|::::|| :|||||  |: ||| :
Db        984 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 1043

Qy        412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
              | | :||||:| ||  :  :||:|:::::||| || | | |: : ::|| :: :  |:
Db       1044 SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 1102

Qy        472 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 531
              |||  :   || : ||: :   :|||:   : |||| ||||||| | ||||||||  | |
Db       1103 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 1162

Qy        532 AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 588
              |||:|   ::|| | ||  |:: : |  ||:   :|:||:||  ||: :|:     :||
Db       1163 AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 1222

Qy        589 STDWSP 594
                :|:|
Db       1223 QYNWTP 1228
```

RESULT 13
US-10-518-599-22
; Sequence 22, Application US/10518599
; Publication No. US20050251873A1
; GENERAL INFORMATION:
; APPLICANT: PENNINGER, JOSEPH M.
; APPLICANT: CRACKOWER, MICHAEL A.
; TITLE OF INVENTION: ACE2 ACTIVATION FOR TREATMENT OF HEART, LUNG AND
; TITLE OF INVENTION: KIDNEY DISEASE AND HYPERTENSION
; FILE REFERENCE: SONN:064US
; CURRENT APPLICATION NUMBER: US/10/518,599
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/CA03/00882
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/389,709
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-518-599-22

Query Match 41.3%; Score 1334; DB 6; Length 732;
Best Local Similarity 42.6%; Pred. No. 1.3e-99;
Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;

```
Qy          2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 61
              | | :|  |:::::  |: |  : : |:| |||||| |  : :     : |    :  |
Db         69 TDEAKADRFVEEYDRTAQVLLNEYAEANWQYNTNITIEGSKILLEKSTEVSNHTLKYGTR 128

Qy         62 AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 121
              |: : :   || ::|  :: ||    :||   : :  | ||  | | ||   :|  :
Db        129 AKTFDVSNFQNSSIKRIIKKLQNLDRAVLPPKELEEYNQILLDMETTYSLSNICYTNG-- 186

Qy        122 ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 181
              |: ||| |  :|| |  | | ||||:||| :||: : | : :||   |::|: | | |
Db        187 TCMPLEPDLTNMMATSRKYEELLWAWKSWRDKVGRAILPFFPKYVEFSNKIAKLNGYTDA 246

Qy        182 GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 240
              || ||  || : ::          :|:|  ::|::||| :||||||  |    | | ||:
Db        247 GDSWRSLYESDNLE----------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 296

Qy        241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
              | :||||||:|| : |:|:| |  ||   |||| |:||: | |  :||||||: || |:
Db        297 DGPIPAHLLGNMWAQTWSNIYDLVAPFPSAPNIDATEAMIKQGWTPRRIFKEADNFFTSL 356

Qy        301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG 359
              ||  :   ||  |||  | : :: ||||:|||   | ||||  || | |:| : |||||||
Db        357 GLLPVPPEFWNKSMLEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMG 416
```

```
Qy        360 HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 419
              |||| | |   |   | ||| |||||:|:||:|| :||||| |: ||| :     | :||
Db        417 HIQYFMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN 475

Qy        420 FLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 479
              ||:| ||  :  :||:|::::||| || | | |: : ::|| :: :  |:  |||  :
Db        476 FLMKMALDKIAFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGD 535

Qy        480 CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM 539
              || | |||  :  ::||:   : |||| ||||:|| | |||||||  | |||: | :
Db        536 FDPGSKFHVPANVPYVRYFVSFIIQFQFHEALCRAAGHTGPLHKCDIYQSKEAGKLLADA 595

Qy        540 LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 594
              ::|| |:||  |:: : |  ||:   ::|||:||  ||  :|:     :||   :|:|
Db        596 MKLGYSKPWPEAMKLITGQPNMSASAMMNYFKPLTEWLVTENRRHGETLGWPEYNWAP 653


RESULT 14
US-10-995-561-1018
; Sequence 1018, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1018
;   LENGTH: 616
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-995-561-1018

  Query Match             39.3%;  Score 1269;  DB 6;  Length 616;
  Best Local Similarity   43.9%;  Pred. No. 1.8e-94;
  Matches  237;  Conservative  100;  Mismatches  185;  Indels   18;  Gaps    7;

Qy         60 TLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDN 119
              | |: : : ::|| |:|  :: :|    : |   : :  | ||  | | ||   ||:|:
Db         12 TQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVATVCHPNG 71

Qy        120 PQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYE 179
                 || ||| |  :|| |  | : ||||| || : |: :    | :|| | |: || | |
Db         72 --SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAARLNGYV 129

Qy        180 DYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY-PSYI 238
              | || ||  ||   ::          :|:|  |:|::||| :|||||  |   |   :|
Db        130 DAGDSWRSMYETPSLE----------QDLERLFQELQPLYLNLHAYVRRALHRHYGAQHI 179

Qy        239 SPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFV 298
              :  | :|||||:|| : |:|:| | |||   |::| |:||: | |  :|:|||: ||
Db        180 NLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKEADDFFT 239

Qy        299 SVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHE 357
              |:||  :   ||  |||  | : :: ||| :|||   | ||||  || | ::| : ||||
Db        240 SLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDLVVAHHE 299

Qy        358 MGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETE 417
              |||||| | |   | || ||| |||||:|::::|| :||||| |: ||| :   | | :
Db        300 MGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGGSD-EHD 358

Qy        418 INFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDE 477
              ||||:| ||  :  :||:|::::||| || | | |: : ::|| ::: :  |:  |||  :
Db        359 INFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRTQ 418

Qy        478 TYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLF 537
              || : ||: :   :|||:   : |||| ||||||| | ||||||||  | ||||:|
Db        419 GDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKEAGQRLA 478

Qy        538 NMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 594
              ::|| | ||  |:: : |  ||:   :|:||:||  ||: :|:     :||   :|:|
Db        479 TAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWPQYNWTP 538


RESULT 15
US-10-995-561-1022
; Sequence 1022, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1022
;   LENGTH: 616
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-995-561-1022

  Query Match             39.3%;  Score 1269;  DB 6;  Length 616;
  Best Local Similarity   43.9%;  Pred. No. 1.8e-94;
  Matches  237;  Conservative  100;  Mismatches  185;  Indels   18;  Gaps    7;

Qy         60 TLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDN 119
              | |: : : ::|| |:|  :: :|    : |   : :  | ||  | | ||   ||:|:
Db         12 TQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVATVCHPNG 71

Qy        120 PQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYE 179
                 || ||| |  :|| |  | : ||||| || : |: :    | :|| | |: || | |
Db         72 --SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAARLNGYV 129

Qy        180 DYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY-PSYI 238
              | || ||  ||   ::          :|:|  |:|::||| :|||||  |   |   :|
Db        130 DAGDSWRSMYETPSLE----------QDLERLFQELQPLYLNLHAYVRRALHRHYGAQHI 179

Qy        239 SPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFV 298
              :  | :|||||:|| : |:|:| | |||   |::| |:||: | |  :|:|||: ||
Db        180 NLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKEADDFFT 239

Qy        299 SVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHE 357
              |:||  :   ||  |||  | : :: ||| :|||   | ||||  || | ::| : ||||
Db        240 SLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDLVVAHHE 299

Qy        358 MGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETE 417
              |||||| | |   | || ||| |||||:|::::|| :||||| |: ||| :   | | :
Db        300 MGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGGSD-EHD 358

Qy        418 INFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDE 477
              ||||:| ||  :  :||:|::::||| || | | |: : ::|| ::: :  |:  |||  :
Db        359 INFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRTQ 418

Qy        478 TYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLF 537
              || : ||: :   :|||:   : |||| ||||||| | ||||||||  | ||||:|
Db        419 GDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKEAGQRLA 478

Qy        538 NMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 594
              ::|| | ||  |:: : |  ||:   :|:||:||  ||: :|:     :||   :|:|
Db        479 TAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWPQYNWTP 538
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Search completed: March 28, 2006, 11:43:16
Job time : 14.1176 secs